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April 21, 2005, 21:13:15; search time 2021.2 Seconds (without alignments) 813.555 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

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7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*

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10: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:*

11: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:*

12: /cgn2_6/ptodata/1/pna/US11_NEW_COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                   OM nucleic - nucleic search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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1041
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	Sequence 3, Appli	Sequence 23, Appl	Sequence 22. Appl	Sequence 4294, Ap	Sequence 1500, Ap	Sequence 1501, Ap	Sequence 5772, Ap	Seguence 5773, Ap		Sequence 3885, Ap	Sequence 8156, Ap	Sequence 8157, Ap	Sequence 37, Appl	38,		Seguence 4310, Ap	Sequence 1, Appli	Sequence 2, Appli	Sequence 6133, Ap	Sequence 4, Appli
SUMMARIES	PCT-US05-03526-3	0 US-11-060-756-23	0 US-11-060-756-22	.0 US-11-060-756-4294	.0 US-11-060-756-1500	.0 US-11-060-756-1501	.0 US-11-060-756-5772	.0 US-11-060-756-5773	.0 US-11-060-756-3884	.0 US-11-060-756-3885	.0 US-11-060-756-8156	0 US-11-060-756-8157	.0 US-11-060-756-37	0 US-11-060-756-38	.0 US-11-060-756-4309	.0 US-11-060-756-4310	PCT-US05-03526-1	PCT-US05-03526-2	US-10-450-763-6133	PCT-US05-03526-4
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10 US-11-060-756-523 10 US-11-060-756-4795 10 US-11-060-756-373 10 US-11-060-756-374 10 US-11-060-756-4645	10 US-11-060-756-4646 9 US-11-085-606-1008 9 US-11-085-606-1012 9 US-11-099-266-92 10 US-11-036-196-1727	10 US-11-060-756-3309 10 US-11-060-756-7581 1 PCT-US05-10257-245 7 US-10-122-851-313 1 PCT-US05-10257-244	8 US-10-450-763-583-1 10 US-11-060-756-241 10 US-11-060-756-242 10 US-11-060-756-4513 10 US-11-060-756-4514	7 US-10-489-448-837 7 US-10-932-182A-81516 2 PCT-USO5-07748-92 7 US-10-525-647-44
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ALIGNMENTS

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RESULT 1		
Sequence 3 GENERAL IN	Sequence 3, Application PC/TUS0503526 GENERAL INFORMATION: APPLICANT: EXPLITE: INC	
TITLE OF	THE STATE OF BRANCHING MORPHOGENESIS AND METHODS 003C-PC	OF 1
CURRENT A	CURRENT APPLICATION NUMBER: PCT/USO5/03526	
PRIOR APP	# 3	
NUMBER OF	FILING DATE: 2004-01-28	
SEQ ID NO	SOFTWAKE: Fatentin Version 3.2 EQ ID NO 3	
LENGTH: 1618	1618 1018	
ORGANISM: Homo	. Homo sapiens	
Query Match	th 70.1%; Score 729.6; DB 2; Length 1618;	
Matches 8	Similarity of.03; Fred. NO. 33; Conservative 0; Mismatc	
λζ	4 GAAAAGTATGAAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAATGC 63	
ob 496	GACCCGTATGAAAAATTAGCTAAGACTGGAGAGGGTCTTATGGGGTTGTATTCAAATGC 555	
<u>و</u>	64 AGAAACAAAACCICTGGACAAGTAGTAGTGTTAAAAAATTTGTGGAATCTGAAGATGT 123	
)b 556		
2y 124	4 CCTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACATCCA 183	
ob 616	CCTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACATCCA 675	
2y 184	4 AATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAGGGAAAATGCATTTAGTTTTTGAA 243	
919 dc	6 AATCTTGTGAACCTCATCGAGGTGTTCAGGAQAAAAGGAAAATGCATTTAGTTTTTGAA 735	
2y 244	4 TACTGTGATCATTGTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGATGGA 303	
3b 736	6 TACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCCAAATGGTATGGATTCTGAC 795	
304	4 GTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACATA 361	

### ATTCCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	RESULT 3 Sequence 4295 Application US/11060756
	0y 946 TCCTACTTTGATTCTTTCAAGAGGCCCAAATTAAAAGAAAAGCGTAATGAAGGAAG

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APPLICANT: Wyeth
APPLICANT: Wounts, William Martin
APPLICANT: Wounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILIA DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PATENTIN VERSION 3.2
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                                                                                                                                                                                                                                                                                                                                                   AAGACGCCAACAGGTACTTCCGCTCAAAAGT 1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 4294, Application US/11060756; GENERAL INFORMATION:
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US-11-060-756-4294
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US-11-060-756-4294
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LENGTH: 600
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GENERAL INFORMATION:
APPLICANT: Wyeth
TAPLICANT: Worth
TITLE OF INVENTION: Target Genes
FILE REPRENCE: AMO1083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT PELICATION NUMBER: US/11/060,756
SOFTWARE: Patentin version 3.2
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                                 CTGATAATCAGAACACTAGTAGAGACGGGGTTTCGCCATGTTGACCAGGCTGGTCTCGAA
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CRGANISM: Homo sapiens
US-11-060-756-22
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APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: Target Genes
FILE REPERENCE: AM101083 (031896-04200)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 1501
LENGTH: 600
                393 ATTAACCTGTTCCCAACTCCTGGAGGCTCCTACTTTGATTCTTTTCAAGAGGCCCAAAT 452
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Pred. No. 1e-67;
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; ORGANISM: Homo sapiens
US-11-060-756-1501
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Best Local Similarity
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US-11-060-756-5772
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TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
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Pred. No. le-67;
0; Mismatches 10; Indels 9
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8-11-060-756-1500
8-11-060-756-1500
Sequence 1500, Application US/11060756
GENERAL INFORMATION:
APPLICANT: Wyeth
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Best Local Similarity 81.9%;
Matches 480; Conservative (
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ORGANISM: Homo sapiens
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Sequence 3884, Application US/11060756
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wheth
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT PILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SEQ ID NO 3884
LENGTH: 1175
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  NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 5773
LENGTH: 600
                                                                                                                                                                      35.4%;
                                                                                                                                                                  Query Match 35.4
Best Local Similarity 81.9
Matches 480; Conservative
                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-5773
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GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
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                                                         APPLICANT: Mounts, William Martin
TITLE OF INVENTION: Nucletc Acid Arrays for Monitoring Expression Profiles
TITLE OF INVENTION: Target Genes
FILE REPERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 5772
LENGTH: 600
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Sequence 5772, Application US/11060756 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   Query Match 35.4%;
Best Local Similarity 81.9%;
Matches 480; Conservative (
                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-11-060-756-5772
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Sequence 8156, Application US/11060756
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William Martin
TITLE OF INVENTION:
TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
FILE REFERENCE: AM101083 (031886-042000)
CURRENT PILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
                                                                                     TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAATTTGTGGAATCTGAAGAT 120
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Best Local Similarity 71.2*
Matches 469; Conservative
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US-11-060-756-8156
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US-11-060-756-8156
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TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target General
TITLE OF INVENTION: Target General
FILE REFERENCE: AM101083 (031896-042000)
CURRENT PAPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
LENGTHARE: DATENTING TARGET SEQ ID NOS 3885
LENGTH: 1175
                                                                                                                                                                                                             TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAATTTGTGGAATCTGAAGAT 120
                                                                                                                                                                                                                                                             TETAGAAACAGGGACAGGGTCAGATTGTGGCCATCAGAAGTTTCTGGAATCAGAAGT 151
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            Pred. No. 1.2e-62;
0; Mismatches 187; Indels
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Pred. No. 1.2e-62;
0; Mismatches 187; Indels
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   71.28;
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                            Matches 469; Conservative
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Best Local Similarity 71.2°
Matches 469; Conservative
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; ORGANISM: Homo sapiens
US-11-060-756-3885
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wyeth
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APPLICANT: Wyeth
APPLICANT: Wounts, William Martin
APPLICANT: Wounts, William Martin
APPLICANT: Wounts, Widleic Acid Arrays for Monitoring Expression Profiles of
TITLE OF INVENTION: Target Genes
FILE REPERENCE: AMI01083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT APPLICATION DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
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                                                                               301 GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
                                                                                                                                                                                                                                               AACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATC 420
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                                                                                                                                                                                                                                                                                     AATTGCATACATAGAGACGTGAAGCCAGAAATATCCTCATCACGAAACATTCCGTGATT 451
                                                                                                                                                                                                                                                                                                                              AAGATTTGTGACTTCGGGTTTGCACAAATTCTGATT---CCAGGAGATGCCTACACCGAT 477
                                                                                                                                                                                                                                                                                                                                                       TATGTAGGTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGT 537
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ATGGCATCAGTATACCTGAGCCAGAAGACATGGAAACTCTTGAGGAAAAGTTCTCAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 27.4%; Score 285.6; DB 10; Length Best Local Similarity 94.3%; Pred. No. 1.4e-50; Matches 283; Conservative 12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 37, Application US/11060756; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-11-060-756-37
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APPLICANT: Wweth
APPLICANT: Weth
APPLICANT: Weth
APPLICANT: Weth
APPLICANT: William Martin
APPLICANT: William Martin
APPLICANT: William Martin
APPLICANT: William Martin
APPLICATION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT PILLIATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 8157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGTGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACACTAGTAGA 656
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                                        GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACAT
                                                                                                    CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAAGGAAAATGCATTTAGTTTTT
                                                                                                                           TATGTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGT
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Pred. No. 1.2e-62;
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Best Local Similarity 71.2
Matches 469; Conservative
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ORGANISM: Homo sapiens
US-11-060-756-8157
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US-11-060-756-38

Sequence 38, Application US/11060756

GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wyeth
TITLE OF INVENTION: Target Genes
TITLE OF INVENTION: Target Genes
TITLE PAPLICANION: Target Genes
TITLE PAPLICANION NUMBER: US/11/060,756
CURRENT APPLICATION NUMBER: US/11/060,756
NUMBER OF SEQ ID NOS: 302284

SOFTWARE PAPLICATION VERSION 3.2
289 AAAGAAAAGCACGTAATGAAGGAAGAACAGAAGACGCCAACAGRWWCWDMBGYTSVCWV 348
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Best Local Similarity 94.3%; Pred. No. 1.4e-50;
Matches 283; Conservative 12; Mismatches 5; Indels 0;
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; ORGANISM: Homo sapiens
US-11-060-756-38
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LENGTH: 600
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Search completed: April 22, 2005, 04:37:03 Job time : 2026.2 secs

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Scoring table:

Searched:

Minimum Maximum

Database

Sequence:

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Run on:

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Tel: 9798452616
Fax: 979845670
Email: davidadelson@tamu.edu.
Location/Qualifiers
1. .695
| Actions is a continued of the cont
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RUGG03000752.R1 CSEQFXN20 testes Bos taurus CDNA, mRNA sequence.
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BY075395 BY075395
AK0950045 Mus muscu
AK050990 Mus muscu
BW352155 BW352155
AK65899 zu89f10.s
CR749116 CR749116
AK046394 Mus muscu
AK046394 AWGNNUC:N
CB732963 AMGNNUC:N
CK7358920 AGENCOURT
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 695)
Adelson, D.L. and Gill, C.A.
Bovine ESTS (Adelson and Gill)
Unpublished (2003)
Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
                                                                                                       AY412141 IBY716459 IBP187523 ICO538154
                                                                BW336241
                                                                                       CK597959
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                                                                                                       AY412141
BY716459
BP187523
CO538154
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BY075395
AX090045
AX050990
BW352155
CR749116
AX046394
AX046394
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CK597959
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Bos taurus (cow)
Bos taurus
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Best Local Similarity
Matches 504; Conserv
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Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-res@gsc.riken.jp, URL.http://genome.gsc.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Pukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
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Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M., anid Hayashizaki,Y.
Direct Submission
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/dev_stage="16 days neonate"
/clone_lib="RIKEN full-length enriched, 16 days neonate
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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85.6%; Pred. No. 4.6e-80;
Live 0; Mismatches 76; Indels
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/db_xref="taxon:10090"
/clone="G630052E12"
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Sakazume, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, W.,
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TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTTGTGGAATCTGAAGAT 120
                                                                                                                              GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACAT 180
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BY733578 RIKEN full-length enriched, 16 days neonate male diencephalon Mus musculus cDNA clone G630052E12 5', mENA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1. (bases 1 to 670)
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BY733578.1 GI:27146705
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 175-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                         1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha,NE 68131 USA ) whose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 ATGGAAAAGTATGAAAAGCTAGCTAAGATCGGAGAAGGGTCTTATGGCGTTGTATTCAAG 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 GATCGTGTCGTTAGGAAAATAGCCCTGCGGAAATCCGTATGCTGAAGCAGTTGAAACAC 348
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                                                                                                                                     Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J., Aizava,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Horri,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="RIKEN full-length enriched, adult inner ear"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp)
further details.
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanaqawa 230-
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/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="F930014I06"
/tissue type="inner ear"
/dev_stage="adult"
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Standard, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N.; Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yadaj, K., Tomaru, Y., Hasqawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batelov, S., Bassel, K., W., Blake, J., Bradt, D., Brusico, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forreet, A., Frazer, K.S., Gaasterland, T., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzlerski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.L., Majott, D.R., Maltas, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Perorokky, N., Pillai, R., Pontius, J.U., Oil, D., Ramachandran, S., Ravasi, T., Read, D.J., Read, J., Randahandran, S., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Taskenaka, Y., Taylor, M.S., Yanagisawa, M., Yang, I., Yang,
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                                                                                                                                 480
              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 500)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="testis"
/dev stage="10-12 week old"
/dab_host==SOLR (Kanamyoin resistant)"
/clone lib="Stratagene mouse testis (#937308)"
/note="Organ: testis, Vector: pBluescript SK-; Site_1:
/note="Organ: testis, Vector: pBluescript St-; Site_1:
/note="Organ: testis, Vector: pBluescript St-; Site_1:
/note="Organ: testis, Vector: pBluescript St-; Site_1: pBluescript St-
                                                                                                                   AAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGATGCCTACACGATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Fax: 314 286 1800
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                                                                                                                                                                                                                         481 GTAGCTACGAGATGGTACCGAGCTCCTGA 509
                                                                                                                                                                                                                                                           648 TGTGCCANCCAGTGGTACCGAGCCCCCGA 676
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/mol_type="mRNA"
/strain="CD-1"
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High quality sequence stop: 339.
Location/Qualifiers
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/clone="IMAGE:513953"
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Best Local Similarity 82.3
Matches 408; Conservative
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AKO16781 adult male testis cDNA, RIKEN full-length enriched library, clone:4933411017 product:cyclin-dependent kinase-like 1 (CDC2-related kinase), full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          494
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                          CCTCATCGAGGTGTTCAGGAGAAAAGGAAAATGCATTTTAGTTTTTGAATACTGTGATCA
                                                                                                                                                              TACACTITITAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGATGGAGTGATCAAAAG
                                                                                                                                                                                                                                                                            315 CGTATTATGGCAAACACTTTCAAGCTCTTAATTTCTGTCATATACATAACTGTATTCACAG
                                                                                                                                                                                                                                                                                                                   179 TGTGCTATGGCAAACCCTTCAAGCCTTAACTTCTGTCACAAGCACAATGTATTCATCG
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                                                                                                                                                                                                                                                                                                                                                                                                Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
9271923
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AK016781.1 GI:12855701
HTC: CAP trapper.
Mus musculus (house mouse)
Mus musculus
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YVATRWYRSPELLVGDTQYGPPVDVWAIGCVFAELLSGVPLWPGKSDVDQLYLIRKTL
BOLLIPHQOYTSMOQYFSGVKIPDPEDMETLELKFPNISYSALGFLKGCLHMDPAERL
TCEQLLQHPYPDSIREVGELTRQHDKPARKTLRQSRKHLTGLQYLPQLTSSRILPALD
NKKYHCSTKRRNYHPNI"
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C_235 Rattus norvegicus cDNA clone
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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                                                                                                                                                                                                                                                                                                                                                     237 TGCAGAAACAGGGACACGGGTCAGATCGTGGCCATCAAGAGGTTTCTGGAAACCGAAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   597 AAGCTCTGTGACTTTGGGTTCGCACGGCTTCTCACTGGACCAGGTGACTACTACACGGAC
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                                                                                                                                                                                                                      1 ATGGAAAAGTATGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                GATCCTGTTGTTAAGAAATAGCACTAAGAAAATACGTATGTTGAAGCAATTAAAACAT
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
                                                                                                                                                                               Gaps
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                                                                                                                                    Length 1691;
                                                                                                                               Score 331, DB 3; Length 16
Pred. No. 1.7e-63;
0; Mismatches 195; Indels
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IMAGE:7110321 5', mRNA sequence.
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ilarity 70.0%;
Conservative
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/db_xref="G1:26382418"
/tb_mref="G1:26382418"
/kramlalet.on="mekyerkigkilgegsygvyfkcrnndtgqivalkrfleteddpvi
KKTALNEIRMLKQLAHPNUVNLLEVFRRRRHLHUVFSYCDHTVLHELDRYQRGVPEPL
VKNITWQTLQAVNFCHKHNCIHRDVKPENILIITKQSAIKLCDFGFARLLTGPGDYYTD
                                                                                                                                                                                                                                                                                                                     Adachi, Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramcto, K., Hiraoka, T., Hordi, P., Inotani, K., Ishli, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okzaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sahai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Noshino, M., Muramatsu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue type="testis"
clone lib="RIKEN full-length enriched mouse cDNA library"
dev_stage="adult"
                                                                                                                                                                                                                      Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
                                                                                        the
                                                                                                                                                                                                 The FANTOM Consortium and the RIKEN Genome Exploration Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="unnamed protein product; cyclin-dependent
kinase-like 1 (CDC2-related kinase) (MGD|MGI:1918341)
                                                                                    The RIKEN Genome Exploration Research Group Phase II Team and
                                                                                                                               Functional annotation of a full-length mouse cDNA collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="FANTOM_DB:4933411017"
/db_xref="taxon:10090"
Genome Res. 10 (11), 1757-1771 (2000)
20530913
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="4933411017"
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/strain="C57BL/6J"
                                                                                                                                                    Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                        (2002)
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                                                                                                        FANTOM Consortium.
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AA061797 ml34h09.rl Stratagene mouse testis (#937308) Mus musculus cDNA ml34h09.rl Stratagene mouse testis (#937308) Mus musculus cDNA clone IMAGE:513953 5' similar to gb:X66358 SERINE/THREONINE-PROTEIN KINASE KKIALRE (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 938)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theişing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                    TACGTGGCCACCAGGTGGTACCGCTCACCTGAGCTGCTAGTGGGAGACACACAGTATGGC 642
                                                                                               538 ICTICAGICGATATAGGGCTATIGGTIGITITIGCAGAGCICCIGACAGGCCAGCCA 597
                                                                                                                                         643 CCCCCAGTAGATGTCTGGGCAATTGGGTGTGTTTGCTGAGTGCTGTCCGGAGTGCCT 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer:
XR Vector;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                th LLNL; contact the further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 GAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACATCCAAATGTTGTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashJ-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.4%; Score 316.8; DB 1; Length 938; 82.9%; Pred. No. 2.5e-60; Live 0; Mismatches 77; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL

IMAGE Consortium (info@image.llnl.gov) for further

MGI:307801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seg primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 442.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .938
/organism="Mus musculus"
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                                                                                                                                                                                                       621
                                                                                                                                                                                                                              CTGTGGCCAGGAAATCGAATGTG 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="IMAGE:513953"
                                                                                                                                                                                               598 CTGTGGCCTGGAAAATCAGATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="CD-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA061797.1 GI:1555606
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                                                                                                                                                                                                                                                                                                                                                                                       / Organism="Acatue norvegicus".
// Mol type="mkNA"
// Ab_xref="taxon:10116"
// Alb_Aref="taxon:10116"
// Alb_Host="MAGE:7110321"
// Lissue type="kidney, pooled"
// Alb_Host="DH10B TonA"
// Alb_Host="Organ: kidney; Vector: pExpress-1; Site_1: EcoRV;
Site_2: Not1; RNA obtained from pooled kidney tissue from a mix of male and female animals at 8 wk old. Tissues were snap-frozen before RNA extraction and purification
(Tri-reagent method). CDNA was primed using oligo-dr primer: 5'-pGACTMGTTCTMAGNCGACGGCCCCC(T)25-3' and cloned into the EcoRV/Not1 sites of pExpress-1.
Size-selection >1.4kb resulted in an average insert size of 2.2 kb. This primary ilbrary is non-normalized (normalized primary library is NHH MGC 236) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MCC 11brary."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       403 ccrciccicaakaakaraacriccacacacacacacacacaraarricroccaraakaa 462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     478 TATGTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGT 537
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Bmail: Gapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Expess Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: WGC clone distribution information can be http://inage.llnl.gov
Plate: LLAM14977 row: e column: 07
High quality sequence stop: 695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGGAAAAGTATGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 TGCAGAAACAGAGACACGGGTCAGCGTGGCCATCAAGAGGTTTCTGGAAAACCGAAGAT
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/organism="Rattus norvegicus"
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Gallus gallus (chicken)

Gallus gallus

Gallus gallus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phaslanidae;

1 (Bases I to 824)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
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gallus cDNA clone ChEST661113 5', mRNA
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                                                                                                                                                                                                                                                                                                                                   547
                                                                                                   TCAAGAAAATCGCGCTGAGGGAAATCAGAATGTTAAAGCAATTGAAACACAATAACTTGG 180
                                                                                                                                                                 TGAACCTCATCGAGGTGTTCAGGAGAAAAGGAAAATGCATTTAGTTTTTGAATACTGTG 250
                                                                                                                                                                                                                          rgaaccrgarrgaagrrinccgrcgaaaacgcaaarracarcirgrgrrcgagrarrgrg 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                371 ACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATCAAGATTTGTG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 ATCGTGATGTAAAACCAGAGAACATATTAATCACTAAGCAAGGTGTTATCAAGTTGTGTG 420
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                                          TTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACATCCAAATCTTG
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Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
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/clone="ChEGT661113"

/tissue_type="whole embryo"

/dev stage="20-21"

/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
1. .824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="CSEQCHN04"
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603750354F1 CSEQCHN04 Gallus
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BU221831
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Fax: 01612360409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AV986182 Nori Satch unpublished cDNA library, larva Ciona intestinalis cDNA clone cilv41b18 5', mRNA sequence.
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1 (basea I to 59%)
Satoh, N., Satou, Y., Kohara, Y. and Shin-i, T.

Expressed genes in Ciona intestinalis
Contact: Nori Satoh
Department of Zoology
CCTCATCGAGGTGTTCAGAAGAAAGAAAGAAGCATCTAGTTTTTGAGTACTGTGATCA 117
                                                                                                                                                                                                                                                              178 TGTGCTATGGCAAACCCTTCAAGCCCTTAACTTCTGTCACAAGCACAATTGTATTCATCG 237
                                                                                                                                                                                                                                                                                                                                                                                                  238 GGATGTAAAACCTGAAAACATCCTAATAACCAAGCAAGGATGATGAAAGATTTGTGAGACT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 TGGATTTGCACGAGTTTCTAATTTCCAGGAGACGCCTACACACAGACTATGTTGCCACCAGGGTG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTACCGAGCCCCCGAACTTCTCGTGGGAGACACGAAGTACGGTTCCTTGTAGACGTGTG 417
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                                                                                                                                                           118 CACACTGTTAAACGAGCTGGAGAAAACCCAAACGGAGTTTCTGATGGAGTGATTAAAAG 177
                                                                                                                                                                                                                             315 CGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACATAACTGTATTCACAG 374
                                                                                                                                                                                                                                                                                                                                                       434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGGTTTGCACAAATTCTGATTCCAGGAGATGCCTACACCGATTATGTAGCTACGAGATG 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGTTCTTCAGTCGATATATG 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 AAACCTCTGGACAAGTAGTAGCTGTTAAAAATTTGTGGAATCTGAAGATGATCCTGTTG 130
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                                                                                                   255 TACACTITIAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGATGGAGTGATCAAAAG
                                                                                                                                                                                                                                                                                                                                                       375 AGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATCAAGATTTGTGACTT
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/clone_lib="Nori Satoh unpublished cDNA library,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kyoto University Sakyo-ku, Kyoto, Kyoto 606-8502, Japan Sakyo-ku, Kyoto, Kyoto 606-8502, Japan Far: 81-75-753-4081
Email: satoh@ascidian.zool.kyoto-u.ac.jp. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Ciona intestinalis"
|mol_type="mkNA"
|do_xref="taxon:719"
|clone="cilv41b18"
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Best Local Similarity 70.7
Matches 423; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 536)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene

Homo sapiens Homo sapiens

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SOURCE
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/note="Organ: whole embryo; Vector: pBluescript II XS(+); Site_1: BcoR1; Site_2: Not!; This normalized library was constructed from I million independent clones. CDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand spathesis reaction. Following this first strand reaction, double-stranded CDNA was blunted, ligated to Notl adapters, digested with ECORI, size-selected, and cloned into the Notl and ECORI compatible sites of a custom modified MCS of the PBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 AAATTIGIGGAATCIGAAGAIGAICCIGTIGITAAGAAATAGCACTAAGAGAAATACGT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220 AGGAAAATGCATTTAGTTTTTGAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 AAGTTCCTGGAGTCCGAGGACCCGGTGATCCGGAAGATCGCGCTGCGGGAGGTCCCC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGTTGAAGCAATTAAAACATCCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 AACCCAAATGGAGTTGCTGATGGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 AGGAAGCTGCACCTGGTCTTTGAGTACTGTGACCACACGCTTCTCCACGAGCTGGACAAG 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 298.4; DB 5; Length 824;
Pred. No. 3.3e-56;
0; Mismatches 191; Indels 3;
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UI-CF-DU1-adn-i-10-0-UI.sl UI-CF-DU1 Homo sapiens cDNA clone UI-CF-DU1-adn-i-10-0-UI.sl UI-CF-DU1 Homo sapiens cDNA clone UI-CF-DU1-adn-i-10-0-UI.s', mRNA sequence. BUG86325.1 GI:23541120 EST.

RESULT 10 BU686325/c LOCUS DEFINITION

ACCESSION VERSION KEYWORDS

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University of lowa
2024 University of lowa Med Labs, lowa City, IA 52242, USA
7024 University of lowa Med Labs, lowa City, IA 52242, USA
7021 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of lowa
CDNA Library preparation: Dr. M. Bento Soares, University of lowa
DNA Sequencing by: Dr. M. Bento Soares, University of lowa
DNA Sequencing by: Dr. M. Bento Soares, University of lowa
Clone Distribution: Researchers may obtain clones from Research
(www.openbiosystems.com) or from Open Biosystems
Seq primer: M13 FORWARD
POLYA-Yes:
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Pred. No. 1.4e-55;
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OSTF177F10_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
CB400506
                                AAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGATGCCTACACGGATTAT
                                               GTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGTTCT
                                                                                       661 GGGTTTCGCCATGTTGACCAGGCTGGTCTCGAACTCTTGACGTCAAGTGATCCACCTGCC
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: Marc_Vidal@dfci.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, E
Tel: 617 632 5180
Fax: 617 632 5739
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Caenorhabditis elegans
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Marc Vidal Laboratory
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AUTHORS
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sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or POLVĀ-No.
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/tissue type="whole animal"
/dev_stage="mixed stage"
/clone lib;="Ab-wrmcDNA"
/note="The Ab-wrmcDNA library was generated with poly(A
RNA isolated from both hermaphrodite and male N2 worms
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNNs by poly(A) priming. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 GCTGTTAAAAAATTTGTGGAATCTGAAGATGATCCTGTTGTTAAGAAAATAGCACTAAGA
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25.9%; Score 269.8; DB 6; Length
Best Local Similarity 67.6%; Pred. No. 8.4e-50;
Matches 379; Conservative 0; Mismatches 182; Indels

    565
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"

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us-10-766-691-9.rst

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 718)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Schellenberg, K., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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TGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACT 364
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Washington University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 315 Cantagram of St. Contagram of St. Cont
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High quality sequence stop: 424.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGTAGATGTCTGGCCAATTGGCTGTGTT 726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 542 CAGTCGATATATGGCTATTGGTTGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .718
/organism="Mus musculus"
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/clone="IMAGE:776337"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
Mus musculus
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/strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA286088.1 GI:1932198
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/lab host="DH10B"
/clone_lib="Sugano mouse kidney mkia"
/clone_lib="Sugano mouse kidney mkia"
/note="Organ: kidney; Vector: pWE18S-FL3; Site_l: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
/AGTGGCCTTTTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and choned into distinct DraII sites of the pWE18S-FL3
vector (5: site CACTGTGTG, 3: site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCACAA."
                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 731)
Marra, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Miderwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Waterston, R. and Wilson, R., The Washul-NcI Mouse EST Project 1999
Umpublished (1999)
Contact: Marra M/Washu-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 AAATATGAAAAAATTGGAAAGATTGGAGAAGGCTCCTATGGGGTAGTGTTCAAGTGCA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 GAAACAAAACCTCTGGACAAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGATGATC 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 CTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACATCCAA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 ATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAGGAAAATGCATTTAGTTTTTGAAT 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 AAAAGTATGAAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGGTTGTATTCAAATGCA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.8%; Score 258.6; DB 2; Length 731; 66.9%; Pred. No. 2.7e-47; arive 0; Mismatches 186; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
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High quality sequence stop: 433.
Location/Qualifiers
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                                                                                           Mus musculus (house mouse)
Mus musculus
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/strain="C57BL"
AW106692
AW106692.1 GI:6077492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="female"
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SOURCE
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AUTHORS
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3']; double-stranded cDNA was ligated to Eco RI adaptors [CATGGATTCGGTACC], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."

ORIGIN

9 ATGGAAAAGTATGAAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA Gaps 7; Query Match 24.5%; Score 255; DB 1; Length 718; Best Local Similarity 67.9%; Pred. No. 1.7e-46; Matches 416; Conservative 0; Mismatches 190; Indels

TGCAGAAACAAAACTCTGGACAAGTAGTAGCTGTTAAAAATTTGTGGAATCTGAAGAT 120 61

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CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAGGAAAATGCATTTAGTTTTT 240 181

289 CCCAACCTGGTCAACCTCCTGGAAGTCTTCCGGAG-AAGCGGAGGCTTCACCTGGTGTTC 347

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TTCTTCAGTCGATATATGGGCTATTGGTTTTTTTGCAGAGCTCCTGACAGGCCAGCC 596 537

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Search completed: April 22, 2005, 01:23:04 Job time: 3334.85 secs

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Sequence 11, Appli
Sequence 5, Appli
Sequence 30, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
                                                                                                                                           April 21, 2005, 23:37:20 ; Search time 3944.37 Seconds (without alignments) 1602.273 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

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22: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-766-691-11
US-10-766-691-11
US-10-766-691-5
US-10-33-314-30
US-10-250-889-6
US-10-766-691-13
US-09-834-496A-3
US-09-834-496A-3
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US-10-766-691-7
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Gapop 10.0 , Gapext 1.0
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ALIGNMENTS

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US-10-766-591-9

US-10-766-591-9

US-10-766-591-9

Publication No. US2005004262641

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Durner, C. Alexander Jr.

APPLICANT: Tried Caredrich, Glenn

APPLICANT: Sands, Arthur T.

TITLE OF INVENTION: Novel Human Kinase Proteins and

TITLE OF INVENTION: NOVEL USA

CURRENT APPLICATION NUMBER: US/09/671,050

PRIOR PRING DATE: 2004-01-28

PRIOR PRING DATE: 1999-09-28

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PASELSEQ for Windows Version 4.0

SEQ ID NO 9

LENGTH: 1041

TYPE: DNA

ORGANISM: homo sapiens

US-10-76-691-9

Query Match

Best Local Similarity 100.0%; Pred. No. 6.6e-266;

Matches 1041; Conservative 0; Misematches 0; Indels 0;
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Gaps

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1 ATGGAAAGTATGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA

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1 ATGGAAAAGTATGAAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGGAAAAGTATGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGG
       Sequence 3, Application US/10766691
Fublication No. US2050042626A1
GENERAL INFORMATION:
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, Glenn
APPLICANT: Sands, Michael
APPLICANT: Sands, Arthur T.
ITILE OF INVENTION: NOVEL Human Kinase Proteins and
TITLE OF INVENTION: NOVEL Human Kinase Proteins and
TITLE OF INVENTION: NOVEL Human Kinase Proteins and
FILE REFERENCE: LEX-0046-USA
CURRENT APPLICATION NOWBER: US/10/766,691
CURRENT APPLICATION NUMBER: US/09/671,050
FRIOR FILING DATE: 2000-09-27
FRIOR APPLICATION NUMBER: US/09/671,050
FRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSRQ for Windows Version 4.0
LENGTH: 1068
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 1025; Conservative
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; ORGANISM: homo sapiens
US-10-766-691-3
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                                                                   901 AIGAATCCAGAIGACAGAITAACCIGITCCCAACTCCTGGAGAGCTCCTACTITGAITCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: INFORMATION:
APPLICANT: HOUTE GENOMICS, INC.; YUE, Henry
APPLICANT: HARALIA, April J.A.; GHANLA, Narinder K.
APPLICANT: HARALIA, April J.A.; CHANLA, Narinder K.
APPLICANT: ARVIZU, Chandra S.; RAMKUNAR, Jayalaxmi
APPLICANT: ARVIZU, Chandra S.; RAMKUNAR, Jayalaxmi
APPLICANT: BUGHRI, Mariah R.; TRIBOULEY, Catherine M.
APPLICANT: THORNTON, Michael B.; BANDMAN, Olga
APPLICANT: THORNTON, Michael B.; BANDMAN, Olga
APPLICANT: BURRORD, Neil; LAL, Preeti G.
APPLICANT: BURRORD, Neil; LAL, Preeti G.
APPLICANT: GREENAMID, Sara R.; TRNG, Y. Tom
APPLICANT: GREENAMID, Sara R.; TANG, Y.; TOM
APPLICANT: WANDER: US 60/220,038
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-08-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 1698381CB1
US-10-333-314-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 30, Application US/10333314
; Publication No. US20030211093A1
; GENERAL INFORMATION;
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TITLE OF INVENTION: Novel Human Kinase Proteins and
TITLE OF INVENTION: Polynucleotides Encoding the Sam;
FILE REFERENCE: LEX-0046-USA;
CURRENT APPLICATION WUMBER: US/10/766,691
CURRENT FILING DATE: 2004-01-28
PRIOR APPLICATION WUMBER: US/09/671,050
PRIOR APPLICATION WUMBER: US 60/156,511
PRIOR APPLICATION WUMBER: US 60/156,511
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASELSEQ for Windows Version 4.0
LENGTH: 972
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
79.1%; Score 823; DB 19;
Best Local Similarity 90.6%; Pred. No. 5.4e-208;
Matches 929; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-691-5
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                                         TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAAGT
                                                                                             GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGAACCCAAATGGAGTTGCTGAT
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                                                                                GATCCTGTTGTTAAGAAAAAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACAT
                                                                                                                                   CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAAGGAAAATGCATTTAGTTTTT
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RESULT 6 US-10-250-889-6

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GENERAL INFORMATION:
APPLICANT: PANZER, SCOLT R; LINCOLM, Stephen E;
APPLICANT: ALTUS, Christina M; DUFOUR, Gerard E;
APPLICANT: JACKSON, Jennifer L; JONES, Adissa L;
APPLICANT: DAM, Tam C; LIU, Tommy F;
APPLICANT: DAMIO, MATCH H; Edward H; PERALTA, Careyna H;
APPLICANT: DAVID, MATCH H; LEWIS, Samantha A.
TITLE OF INVATION: WOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVATION: WOLEST: USO
CURRENT FILING DATE: 2003-07-09
FRIOR PAPLICATION NUMBER: US 60/261,622
PRIOR PAPLICATION NUMBER: US 60/261,622
PRIOR PAPLICATION NUMBER: US 60/261,864
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US 60/262,208
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US 60/262,205
PRIOR PELING DATE: 2001-01-17
PRIOR PELING DATE: 200 73.3%; Score 762.8; DB 18; Length 1678; 90.0%; Pred. No. 7.1e-192; tive 0; Mismatches 2; Indels 101; NAME/KEY: misc_feature OTHER INFORMATION: Incyte ID No: LI:058298.1:2001JAN12 Query Match
Best Local Similarity 90.0°
Matches 925; Conservative ORGANISM: Homo sapiens 8 ø

Fri Apr

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TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAATTTGTGGAATCTGAAGAT 120
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                                                                                                       Score 709; DB 19;
Pred. No. 1.5e-177;
0; Mismatches 0;
               FastSEQ for Windows Version 4.0.
                                                                                                                                0;
                                                                                                   Query Match 68.1%;
Best Local Similarity 77.0%;
Matches 1025; Conservative (
                                                  TYPE: DNA
ORGANISM: homo sapiens
US-10-766-691-13
            SOFTWARE: FastS
SEQ ID NO 13
LENGTH: 1819
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Publication No. US20050042626A1
GENERAL INFORMATION:
APPLICANT: Donnho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Priedrich, Glenn
APPLICANT: Arbis Michael
TITLE OF INVENTION: Polynuclectides Encoding the Same
FILE REFERENCE: LEX-0046-USA
CURRENT APPLICATION NUMBER: US/10/766,691
FILE REPLATION NUMBER: US/09/671,050
PRIOR FILING DATE: 2000-09-27
PRIOR PILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
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TITLE OF INVENTION: 14257 NOVEL PROTEIN KINASE MOLECULES AND
TITLE OF INVENTION: 14257 NOVEL PROTEIN KINASE MOLECULES AND
TITLE OF INVENTION: 14257 NOVEL PROTEIN KINASE MOLECULES AND
FILE REFERENCE: 31552000900
CURRENT APPLICATION NUMBER: US/09/834,496A
CURRENT FILING DATE: 2001-04-13
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09834496A
Patent No. US20020090701A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) NAME/KEY: CDS
; LOCATION: (129)...(815)
US-09-834-496A-1
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GURRENT APPLICATION NUMBER: 08/09/834,496A
CURRENT PILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/196,910
PRIOR APPLICATION NUMBER: 60/196,910
PRIOR APPLICATION NUMBER: 60/196,910
SEQUID NOS: 7
SOFTWARE: PASTESEQ for Windows Version 4.0
SEQUID NO 3
LENGTH: 687
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Pred. No. 6.2e-161;
0; Mismatches 4;
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Best Local Similarity 99.4
Matches 648; Conservative
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ORGANISM: Homo sapiens
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                      GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT
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Pred. No. 3.7e-110;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nehls, Michael
APPLICANT: Sender, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
ITLLE OF INVENTION: Novel Human Kinase Proteins and
ITLLE OF INVENTION: Novel Human Kinase Proteins and
ITLLE OF INVENTION: Novel Human Kinase Proteins and
ITLLE OF INVENTION: Doyle 1934
CURRENT FILING DATE: 2004-01-28
FRIOR FILING DATE: 2006-09-27
FRIOR PELING DATE: 1999-09-28
FRIOR PELING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
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FRIOR FILING DATE: 1090-09-27
FRIOR FILING DATE: 1090-09-27
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FRIOR FILING DATE: 1090-09-28
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FRIOR FILING DATE: 1090-09-29
FRIOR FILING DATE: 1090-09-29
FRIOR FILING DATE: 1090-
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Best Local Similarity 99.8°
Matches 455, Conservative
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; ORGANISM: homo sapiens
US-10-766-691-7
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APPLICANT: Domono, Gregory
APPLICANT: Domono, Gregory
APPLICANT: Nehls, Michael
APPLICANT: Nehls, Michael
APPLICANT: Riddrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands Arthur T.
TITLE OF INVENTION: Novel Human Kinase Proteins and
TITLE OF INVENTION: Polynuclectides Encoding the Same
FILE REFERENCE: LEX-0046-USA
CURRENT APPLICATION NUMBER: US/09/671,050
PRIOR PELICATION NUMBER: US/09/671,050
PRIOR PELICATION NUMBER: US/09/671,050
PRIOR APPLICATION NUMBER: US 60/156,511
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENTH: S61
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43.7%; Score 454.4; DB 19;
Best Local Similarity 99.8%; Pred. No. 3.6e-110;
Matches 455; Conservative 0; Mismatches 1;
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Publication No. US20050042626A1
GENERAL INFORMATION:
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ORGANISM: homo sapiens
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US-10-766-691-1
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Qy 478 TATGTAGCTACGAGATGCTAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGT 537 Db 697 TACGTGGCTACCAGGTGCTCCCCTGAGCTGCTGGTGGGAGACACGCAGTACGGC 756 Qy 538 TCTTCAGTCGATATATGGGCTATTGGTTGTTTTTGCAGAGCTCCTGACAGGCCAGCA 597 Db 757 CCCCGGTGATATTGGCTAGTGTTTTTTGCAGAGCTGCTGTCAGAGGTGCT 816 Qy 598 CTGTGGCCTGGAAATCAGATGGCACTTATCTGATAATCAGAACACTAGTAGA 656 Bb 679 CTGTGGCCTGGAAAATCAGATGTGCACAACTTTATCTGATAATCAGAACACTAGTAGA 656 Bb CTGTGGCCTGGAAAATCAGATGTGCACCAACTTTATCTGATAATCAGAACACTAGTAGA 656 CTGTGGCCTGGAAAATCAGATGTGGATCAGCTGTTAATCTGATAACGAACACTTAGTAGA 656 Bb 617 CTGTGGCCAGGAAAATCGGATGTGGATCAGCTGTATATCTGATAACGAACACTTGGGGGA 875	13 6.3-616-146	Similarity 71.2%; Pred. No. 1.5e-80; John Stronger, Conservative 0; Mismatches 187; Indels ATGGAAAAGGGTCTTATGGGG	Db 466 ATGGAGAAGTATGAAAAATTGGGAAAATTGGGAAGGATCCTATGGATTTCAAA 525 Qy 61 TGCAGAAACTCTGGGAAAGTAGTAGTAGTAGTAAAAATTTGTAAAATTTGTGAAGATTGAAAAT 120	Db 526 IGTRIGARACAGGGACACCGGGTCAGATTCTCAGAAGTTCTGGAATCAGAAGT 585 Qy 121 GATCCTGTTAAGAAATAGCACTAAGAGAAACGTTGAGGGAATTAAAACAT 180		Db 646 CCCAACCTTGTTAACCTCCTGGAAGTCTTCAGGAGGAAACGGAGGCTTCACCTGGTGTTT 705 Qy 241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAA	Db 706 GAATALTOTGACCACAGTTCCCATGAGTTCCAAGACAGACAAACCAAAGAGGGGGGGAAA 765 Qy 301 GGAGTGATCAAAAGCGAATTATGGCAAACACTTCAAGCTCTAAATTTCTGTCATATAAAT 360	Db 766 CATCTCGTGAAGAGCATAACTTGGCAGACACTGCAAGCTGTAAATTTTTGCCATAAACAC 825	ANTIGATICA CARACTATA ANTACA CONTRACTATA CARACTATA CARACTATA CATAGA ANTACATA CATACATA CATACATA CATACATA CATACATA	Oy 421 AAGATTIGIGACTTIGGGTTTIGCACAAATTCTIGATTCCAGGAGATGCCTACACGAT 477	478
	RESULT 12 US-09-960-706-1079 is Sequence 1079, Application US/09960706 is Sequence 1079, Application US/09960706 is Publication No. US20030134280A1 is Publication No. US20030134280A1 is Publication No. US20030134280A1 is APPLICANT: William E. is TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplae is TITLE OF INVENTION: Gene Expression Profiles is TURENT FILING DATE: 2001-09-24 is PRIOR APPLICATION NUMBER: 60/223,323 is PRIOR PILING DATE: 2000-08-07 is PRIOR PILING DATE: 2001-06-05 is NUMBER OF SEQ ID NOS: 1124 is SEQ ID NO 1079 is LENGTH: 1363 is TYPE: DNA ordanism: Homo sapiens is FEATURE: is OTHER INPORMATION: Genbank Accession No. US20030134280A1 X66358	2	Qy 1 AIGGAAAAGIAIGAAAAATIAGCIAAGACIGGAGAAGGGICTIAIGGGGTIGIATICAAA 60 	OY 61 TGCAGAAACAAAACCTCTGGACAAGTAGTAGTTGTTAAAAATTTGTGGAATCTGAAGAT 120 Db 277 TGTAGAAACAGGGACACGGGTCAGATTGTGGCCATCAAGAAGTTTCTGGAATCAGAAGAT 336	OY 121 GATCCTGTTGTTAAGAAAATAGCACTAAGAAATACGTATGTTGAAGCAATTAAAACAT 180	Qy 181 CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAAGGAAAATGCATTTAGTTTTT 240	Qy 241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGAACCCAAATGGAGTTGCTGAT 300	Oy 301 GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATCAT 360	361 AACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGAAGAATATC 161 HACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATC	Db 577 AATTGCATACATAGAGACGTGAAGCCAGAAAATATCCTCATCACGAAACATTCCGTGATT 636 Ov 421 AAGATTTGGACTTTGGACAAATTCTGAAATTCTGAGAAGATGCCTACACGAT 477	637 AAGCTTTGTGACTTTGGACTTTTGACTGGACCGAGTGACTATACAGAC

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1069 GAATATTGTGACCACACACATTCTCCATGAGTTGGACAGATACCAAAGAGGGGTACCAGAA 1128
                                                                                                                                       1249 AAGCTITIGIGACTITIGGATTIGGTCGGCTTTTIGACTGGACCGAGTGACTACTATATACAGAC 1308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/10174794
; Sequence 5, Application US/10174794
; Publication No. US20030166220A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOWIC, AND PREDICTED PROTEIN
; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES;
; FILE REPERENCES: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174,794
; CURRENT FILING DATE: 1999-10-01
; PRIOR FILING DATE: 1999-10-01
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FRAESEQ for Windows Version 4.0
; FROM THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF THE OF T
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; ORGANISM: Orcytolagus cuniculus
US-10-174-794-5
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Matches 407; Conservative
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GENERAL INFORMATION:

APPLICANT: Schlegel. Robert

APPLICANT: Schlegel. Robert

APPLICANT: Endege, wilson

APPLICANT: Endege, wilson

TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR

TITLE OF INVENTION: HUMAN PROSTATE CANCER

TITLE OF INVENTION: HUMAN PROSTATE CANCER

TITLE OF INVENTION: HUMAN PROSTATE CANCER

TITLE OF INVENTION: HUMAN PROSTATE CANCER

TITLE OF INVENTION: HUMAN PROSTATE CANCER

FILE REFERENCE: MRI-007BCN

CURRENT FILING DATE: 2003-02-04

PRIOR APPLICATION NUMBER: 60/189,862

PRIOR FILING DATE: 2000-03-16

PRIOR PELING DATE: 2000-03-16

PRIOR PELING DATE: 2000-05-25

PRIOR PELING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 60/211,314

PRIOR FILING DATE: 2000-05-28

PRIOR PELING DATE: 2000-05-18

PRIOR FILING DATE: 2000-05-18

PRIOR PELING DATE: 2000-12-18

SEQ ID NO 24573

LENGTH: 2944
946 TACGTGGCTACCAGGTGGTACCGCTCCCCTGAGCTGGTGGGGGACACGCAGGAACGC 1005
                                                                                                                             1006 ccccccciadarciridadcaairidacidircriridendacidendacidadanadeen 1065
                                                                1009 cccaaccrrerraaccrccresaacrcrrcaesagaaacesagacrrcacresrerrr 1069
                                                                                                                                                                                         598 CTGTGGCCTGGAAATCAGATGTGGACCAACTTTATGTGATAATCAGAACACTAGTAGA 656
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LOCATION: 1, 2, 3, 2940, 2941, 2942, 2943, 2944
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24573, Application US/10357930
Publication No. US20040259086Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-357-930-24573
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301 GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360

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421 AAGATTTGTGACTTTGGGGTTTGCACAAATTCTG---ATTCCAGGAGATGCCTACACCGAT 477

361 AACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATC 420

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Search completed: April 22, 2005, 06:44:17 Job time : 3951.37 secs

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Sequence 11, Appl
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Sequence 17, Appli
Sequence 67, Appli
Sequence 5, Appli
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Sequence 9, Appli
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Sequence 114, App
Sequence 114, App
Sequence 2154, Ap
Sequence 3, Appli
Sequence 115, App
Sequence 4905, Ap
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Seguence 3, Appli
                                                                                      April 21, 2005, 20:27:40; Search time 197.088 Seconds (without alignments) 8642.674 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-411-628-5
US-10-174-794-5
US-09-411-628-3
US-09-494-016-2083
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US-08-874-347-9
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US-09-220-132-3
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US-09-266-225D-13
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Maximum Match 100%
Listing first 45 summaries
                                                           - nucleic search, using sw model
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APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nichels, Michael
APPLICANT: Sambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Sambrowicz, Brian
APPLICANT: No. 67166161 Human Kinase Proteins and
TITLE OF INVENTION: No. 67166161 Human Kinase Proteins and
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TITLE OF INVENTION: NO. 67166161 Human Kinase Proteins and
TITLE OF INVENTION NUMBER: US/09/671,050
CURRENT FILING DATE: 2001-06-11
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
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GENERAL INFORMATION:
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; Sequence 5, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
APPLICANT: Denie, Michael
; APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Tradarich, Glenn
; APPLICANT: Sands, Arthur T.
TILE OF INVENTION: No. 6716616e1 Human Kinase Proteins and
TITLE OF INVENTION: No. 6716616e1 Human Kinase Proteins
; TILE OF INVENTION: No. 6716616e1 Human Kinase Proteins
; TILE OF INVENTION: No. 6716616e1 Human Kinase Proteins
; FILE OF INVENTION: No. 6716616e1
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/09/671,050
; CURRENT APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SCO ID NO 5
; LENGTH. 972
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90.6%; Pred. No. 1.2e-223;
iive 0; Mismatches 0;
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Matches 929; Conservative
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GRGANISM: homo sapiens
US-09-671-050-5
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                       361 AACTGTATTCACAGAGATATAAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATC 420
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Pred. No. 3.5e-228;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                    GENERAL INTORNATION:
APPLICANT: Donoho, Gregory
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Reiedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Sambrowicz, Brian
APPLICANT: Brian
APPLICANT: Brian
APPLICANT: Bolymuclectides Encoding the Same
FILE REFERENCE: LEX-0046-USA
CURRENT APPLICATION NUMBER: US/09/671,050
CURRENT APPLICATION NUMBER: US 60/156,511
PRIOR PILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 945
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Best Local Similarity 90.8
Matches 945; Conservative
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CORGANISM: homo sapiens
US-09-671-050-11
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61 TGCAGAAA 61 TGCAGAAA 121 GATCCTGT 121 GATCCTGT 181 CCAAATCT		301 GGAGTGATC 361 AACTGTATT	421 AAGATTTGT 421 AAGATTTGT	481 GTAGCTACG 481 GTAGCTACG	541 TCAGTCGAT 541 TCAGTCGAT	601 TGGCCTGGA 601 TGGCCTGGAA	661 GGGTTTCGCC		721 GTAGCCTCTC 651	781 AAAAGTAACG		841 GAGGAAAAGT 745 GAGGAAAGT	901 ATGAATCCAG				CAGGT	925 CAGGT 929	RESULT 5 US-09-671-050-13	e 13, Applicatio
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61 TGCAGAACAAAACCTCTGGACAAGTAGTGTTTAAAAAATTTGTGGAATCTGAAGAT 120 121 GATCTGTTGAAAAAAAAAGCACTAAGAAAATACGTATGTTGAAGGAATTAAAACAT 180 1 ATGGAAAAGTATGAAAAATTAGCTAAGACTGGAAAGGGTCTTATGGGGTTGTATTCAAA 60 454 ----- 453 618 ICCITGATIGGCTTAAIAGTIGACCTICTGAAITCTTTTTTTGGCCAATTCAGAGAITTTT 677 454 ----- 453 678 CTCCTGGCTTGGATCCATTGCTGACAGTGTTTCACCATGGGGCCCCAGGCTCATCTCGA 737 738 ACTICIGGCCICAAGIGAICCTICCACCICGGCCTCCCAAAGIGCTGGAITGCAAGIGIG 797 0; Indels 306; Gaps 421 AAGAITTGTGACTTCGGGTTTGCACAAATTCTG------GENERAL INFORMATION:
APPLICANT: Donoho, Gregory
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Reiderich, Gleun
APPLICANT: Zambrowicz, Gleun
APPLICANT: Zambrowicz, Brian
APPLICANT: Zamds, Arthur T.
TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
TITLE OF INVENTION: Polynucleotides Encoding the Same
TITLE OF INVENTION: Polynucleotides Encoding the Same
CURRENT APPLICATION NUMBER: US 60/9671,050
FRIGH SPPLICATION NUMBER: US 60/156,511
PRIOR FILING DATE: 1999-09-28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ 1D NO 13
LENGHH: 1819 Nuery Match 68.1%; Score 709; DB 4; Length 1819; Set Local Similarity 77.0%; Pred. No. 4e.191; latches 1025; Conservative 0; Mismatches 0; Indels 30 TYPE: DNA ORGANISM: homo sapiens 09-671-050-13 454 ----g ઠે ö

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61 TGCAGAAACAAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
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      Length 561;
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APPLICANT: Nehls, Michael
APPLICANT: Nehls, Michael
APPLICANT: Friedrich, Glenn
APPLICANT: Friedrich, Glenn
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REPERENCE: LEX-0046-USA
CURRENT APPLICANT: 2001-06-11
                                            Indels
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    DB 4;
    Score 454.4; DB 4;
Pred. No. 4.1e-119;
0; Mismatches 1;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 594
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PRIOR APPLICATION NUMBER: US 60/156,511
PRIOR FILING DATE: 1999-09-28
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    43.78;
Query Match
Best Local Similarity 99.8
Matches 455; Conservative
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Best Local Similarity 99.8
Matches 455; Conservative
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    798 AGCCACCGTGCCCAGCCAGATTTTTCAAACAATAACTACTGAGAGCTCACAAGATTGTTT 857
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                                                                    475 GATTATGTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTAT
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APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nehls, Michael
APPLICANT: Nehls, Michael
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6716616e1 Human Kinase Proteins
TITLE OF INVENTION: Polynucleotides Encoding the Same
PILE REPERENCE: LEX-0046-USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/671,050
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: US 60/156,511
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FRASEQ for Windows Version 4.0
SEQ ID NO 1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09671050
Patent No. 6716616
GENERAL INFORMATION:
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CRGANISM: homo sapiens
US-09-671-050-1
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US-09-411-628-5

i Sequence 5, Application US/09411628

sequence 6. 642894

GENERAL INFORMATION:

TITLE OF INVENTION: CDMA, GENCMIC, AND PREDICTED PROTEIN

TITLE OF INVENTION: CDMA, GENCMIC, AND PREDICTED PROTEIN

TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES;

CURRENT APPLICATION NUMBER: US/09/411,628

EARLIER PILING DATE: 1999-10-01

MUNBER OF SEQ ID NOTE: 1998-10-02

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 1701
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                                                                                                                                                                                                                                                                 AAGATTTGTGACTTCGGGTT
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US-09-411-628-5
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Fatent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
FRIOR FILING DATE: 2000-10-20
FRIOR PELICATION NUMBER: 60/241,755
FRIOR FILING DATE: 2000-10-03
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRAILS 2000-10-03
SOFTWARE: FRAILS 2000-10-04
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33.0%; Score 343.8; DB 4;
Best Local Similarity 71.2%; Pred. No. 1.5e.87;
Matches 469; Conservative 0; Mismatches 187;
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US-09-949-016-1681
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US-09-949-016-1681
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                     301 CAAGTAGTTCAAAAGTATTTGTTTCAGATTATTAATGGAATTGGATTTTGTCACAGTCAC 360
                                                                    AACTGTATTCACAGAGATATAAAACCTGAAATATTCTAATAACTAAGCAAGGAATAATC 420
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APPLICANT: University of Southern California
APPLICANT: University of Southern California
TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
FILE REFERENCE: 13761-707
CURRENT APPLICATION NUMBER: US 60/411,628
CURRENT FILING DATE: 1999-10-01
EARLIER APPLICATION NUMBER: US 60/102,906
BARLIER FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FREESEQ for Windows Version 4.0
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Patent No. 6428994
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LOCATION: (249)...(1949)
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LENGTH: 3080
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GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT
                                                                                          AACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATC
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Patent No. 6664086

GENERAL INFORMATION:
TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
FILE REFERENCE: 13761-707
CURRENT APPLICATION NUMBER: US/10/174,794

CURRENT APPLICATION NUMBER: US/09/411,628

PRIOR PALICATION NUMBER: US 60/102,906

PRIOR PALLING DATE: 1999-10-01

PRIOR PILING DATE: 1999-10-01

PRIOR PILING DATE: 1999-10-01

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FASTESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGTGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAG 644
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Sequence 2083, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| CURRENT APPLICATION NUMBER: US/09/949,016
| PRIOR PELING DATE: 2000-04-14
| PRIOR PILING DATE: 2000-10-20
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SOFFWARE: FREISEQ FOR WINDOWS VERSION 4.0
                                            301 GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
                                                                                  549 Caádhaghrcáaáagnanhartaahnahhaahhagaahhrighdacagndac 608
                                                                                                                                                                609 AATATCATACATAGAGATATAAAGCCAGAGAATATATTGGTCTCCCAGTCTGGCGTTGTC 668
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Pred. No. 2.5e-58;
0; Mismatches 243;
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Best Local Similarity 61.9%;
Matches 400; Conservative (
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                                                                                                                                                                                      AAGTTATGTGATTTTGGATTTTGCACGGACACTGGGCAGCTCCCGGAGAGGTTTACACTGAT
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GENERAL INFORMATION:

APPLICANT: University of Southern California

TITLE OF INVENTION: EDWA, GENOMIC, AND PREDICTED PROTEIN

TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES

FILE REFERENCE: 137-61-707

CURRENT APPLICATION NUMBER: US/10/174,794

CURRENT FILING DATE: 2002-06-18

PRIOR APPLICATION NUMBER: US/09/411,628

PRIOR PILING DATE: 1999-10-01

PRIOR PLING DATE: 1999-10-02

NUMBER OF SEQ ID NOS: 16

SOFTWARR: FABESEQ for Windows Version 4.0

SEQ ID NO 3: SEQ ID NOS: 16
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Patent No. 6664086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Orcytolagus cuniculus
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 62.9'
Matches 407; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (249)...(1949)
US-10-174-794-3
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Query Match
Best Local Similarity 55.2%;
Matches 365; Conservative
; OTHER INFORMATION:
US-08-874-347-9
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   GAATTTGTTGACCACACAATTCTTGATGACTTGGAGCTCTTTCCAAATGGACTAGACTAC 675
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                                  301 GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT
                                                                caagiagircaaaagrariigirrcagarrariiaarggaariiggarirrigicagagrad
                                                                                               361 AACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATC
                                                                                                                AAGATTTGTGACTTCGGGTTTGCACAAATTCTG---ATTCCAGGAGATGCCTACACCGAT
                                                                                                                                                                                            AAGCTATGCGATTTTGGATTTGCGCGAACATTGGCCAGCTCCTGGGGGGGTTTATACTGAT
                                                                                                                                                                                                                             TATGTAGCTACGAGATGCTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGT
                                                                                                                                                                                                                                                           Sequence 9, Application US/08874347

Patent No. 5863741

GENERAL INFORMATION:
APPLICANT: Limper, Andrew H.
APPLICANT: Thomas, Charles P.
APPLICANT: Thomas, Charles P.
TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS
TITLE OF INVENTION: CARINII
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS: 26
CORRESPONDENCE ADDRESS: 36
TREET: 60 South Sixth Street, Suite 3300
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                        CTATTTCCTGGAGATTCTGATATTGATCAGCTATATCATATTATGA 1021
                                                                                                                                                                                                                                                                                                                                                         CTGTGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: F8815EG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,347
FILING DATE: 13-70N-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07039/055001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ellinger, Mark S. REGISTRATION NUMBER: 34,812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 0
TELECOMMUNICATION INFORMATION
TELEPHONE: 612-335-5070
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SEQUENCE CHARACTERISTICS:
LENGTH: 903 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 612-288-9696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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LOCATION:
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| Patent No. 6015700
| GENERAL INFORMATION:
| APPLICANT: Limper, Andrew H. APPLICANT: Limper, Andrew H. APPLICANT: Leof, Edward B. APPLICANT: Thomas, Charles F. APPLICANT: TOCK Gustafson, Michael P. TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS TITLE OF INVENTION: CARINII NUMBER OF SEQUENCES. 26
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Fish & Richardson P.C., P.A. CITY: Minneapolis
    Length 903;
Score 163.8; DB 2; Length
Pred. No. 1.6e-36;
0; Mismatches 287; Indels
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          COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/093,522
FILING DATE: 08-JUN-1998
PRIOR APPTICATION:
                                                                                                                                                                                                                                                                                                                                                                                                07039/055002
                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/874,347
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                        NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
REFERENCE/DOCKET NUMBER: 0703
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-335-5070
TELEPHONE: 612-288-9696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: Coding Sequence
; LCCATION: 1...900
; OTHER INFORMATION:
US-09-093-522-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 901 base pairs
LYPE: nucleic acid
STRANDEDNESS: single
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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Ado01535 Human cyc Aby93433 Human cDN Abv24584 Human pro Aaa29745 Rabbit KK Aaa29745 Rabbit KK Abl12603 Drosophil Adc7568 Human 162 Adg9155 Human 103 Adf57213 Human 108 Adf57213 Human NKI Aa806724 Polynucle Ach12602 Drosophil Aax51207 Rat lost Aax51207 Rat lost Aax51207 Rat lost Aax51207 Rat lost Aax51207 Rat lost Aax51207 Rat lost Aax51307 Rat lost Aax51307 Rat lost Aax1073 Crosophil Aay71073 Cyclin-de Aav71073 Cyclin-de Aav71073 Cyclin-de Aav71073 Cyclin-de Aav71073 Cyclin-de Aby66075 Human Cyc

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Location/Qualifiers
1: .1041
/*tag= a
/product= "Human kinase #5"
/note= "The coding region does not include stop codon"
/partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated human kinase polynucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Friedrich G, Zambrowicz B;
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                                   AAA29745
ABL12603
ADC77658
ADQ89155
AAZ51208
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AAX07476
AAZ37835
                                                                                 ADI57213
AAS06724
ACN42574
AAZ51207
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ABZ83372
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ADD21391
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ABL12602
AAS70329
AAF44672
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                                                                                                                                                                                                                                                                                                      AAD03816 standard; cDNA; 1041 BP
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P-PSDB; AAE00494.
WO200123579-A1
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Sands AT;
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251.8
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186.6
177.4
175.2
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Aad03817 Human kin
Aad03817 Human kin
Aad30557 Human kin
Aad30557 Human kin
Aad30557 Human kin
Aas06725 Polymucle
Aad03818 Human kin
AdX71927 Human kin
AdX71927 Human kin
AdX4679 Human kin
Aat44669 Novel pro
Ad129367 Human kin
Aad03812 Human kin
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                                                               April 21, 2005, 20:23:24; Search time 569.772 Seconds
(without alignments)
10815.645 Million cell updates/sec
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                                                                                                                        1 atggaaaagtatgaaaaatt......aggtacttccgctcaaaagt 1041
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        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                     4390206 seqs, 2959870667 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                              OM nucleic - nucleic search, using sw model
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AAD30557
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AAC0836
AAC06725
AAD03818
ADK71927
AAT64248
AD129367
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AAD03812
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AAD03817
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                                                                                                                                        IDENTITY NUC Gapop 10.0 , Gapext 1.0
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Score

Result No.

1041 1025 839 823 821 762.8 757 709 709 702 644 604 604 537 537

454.4 454.4 453.2 453.2 343.8

Minimum DB seq Maximum DB seq

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Database

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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The diagnosts of disease, and also as a therapeutic. It is useful for acreening drugs effective in the treatment of symptomatic or phenotypic acreening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of MHP in the body. The MHP mucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the identification of other cellular gene products related to human kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical disorders. MHP oligonucleotides are used as probes. The labelled NHP probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP produces are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression
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The present sequence is a cDNA encoding novel human protein (NHP) known as human kinases. The human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGGAAAAGTATGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 1041; DB 4;
Best Local Similarity 100.0%; Pred. No. 9.9e-268;
Matches 1041; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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1/trag= a froduct= "Human kinase #2"
foroduct= "The coding region does not include stop codon"
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                                                                         AAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAAGACATGGAAACTCTT
                                                                                     AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAAGACATGGAAACTCTT
                                                                                                                                   GAGGAAAAGTTCTCAGGTTCATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAG
                                                                                                                                                                         ATGAATCCAGATGACAGATTAACCTGTTCCCAACTCCTGGAGGGCTCCTACTTTGATTCT
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biological disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                    (first entry)
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The present sequence is a cDNA encoding novel human protein (NHP) known as human kinase. The human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases.
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/product= "Human kinase #6"
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                                        GTAGCCTCTCAAAGTGCTGGAATTACAGGAAAATTAATCCCAAGACATCAATCTTT
                                                                                                                                                   GAGGAAAAGTTCTCAGATGTTCATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAG
                                                                                                                                                                       GAGGAAAAGITTCTCAGATGTTCATCCTGTGGCTCTGAACTTCATGAAGGGGGTGTCTGAAG
                                                                                     AAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAAGACATGGAAACTCTT
                                                                                                                   AAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCCAGAAGACATGGAAACTCTT
                                                                                                                                                                                                                 ATGAATCCAGATGACAGATTAACCTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTCT
                                                                                                                                                                                                                                New isolated human kinase polynucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases.
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P-PSDB; AAE00495.
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100.0%; Pred. No. 1.9e-263;
vative 0; Mismatches 0;
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Matches 1025; Conservative
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Sequence 945 BP; 323 A; 165 C; 202 G; 255 T; 0 U; 0 Other;

96; Gaps Best Local Similarity 90.8 Matches 945; Conservative Query Match

9 1 ATGGAAAAGTATGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA

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099 TGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACACTAGTAGAGACG 501 TGGCCTGGAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACACT-----601

GGGTTTCGCCATGTTGACCAGGCTGGTCTCGAACTCTTGACGTCAAGTGATCCACCTGCC 720

721

744 960 -----AGGAAAATTAATCCCAAGACATCAATCTTT 684 GAGGAAAAGTTCTCAGATGTTCATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAG ATGAATCCAGATGACAGATTAACCTCTTCCCAACTCCTGGAGAGGTCCTACTTTGATTCT TITCAAGAGGCCCAAAITAAAAGAAAAGCACGTAATGAAGGAAGAAGAAGAAGAAGACGCCAA GAGGAAAAGTICTCAGATGTTCATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAG AAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAAGACATGGAAACTCTT 805 ATGAATCCAGATGACAGATTAACCTGTTCCCAACTCCTGGAGGCTCCTACTTTGATTCT CAGGTACTTCCGCTCAAAAGT 1041 CAGGTACTTCCGCTCAAAAGT 945 1021 925 781 685 841 745 901 651 196 g g 셤 8 à ò g 8 ઠ

AAD03814

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BP AAD03814 standard; cDNA; 972

AAD03814;

(first entry) 19-JUN-2001

Human kinase cDNA #3.

Human; kinase; gene therapy; bioreactor; mental disorder; biological disorder; ss.

Homo sapiens

1. .972 /*tag= a /product= "Human kinase #3" /note= "The coding region does not include stop codon" /partial Location/Qualifiers

WO200123579-A1

05-APR-2001,

27-SEP-2000; 2000WO-US026621.

28-SEP-1999;

(LEXI-) LEXICON GENETICS INC

m Zambrowicz Friedrich G, Donoho G, Turner CA, Nehls M, Sands AT;

WPI; 2001-266166/27. P-PSDB; AAE00492. New isolated human kinase polynucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases.

Disclosure, Page 29-30; 38pp; English.

for The present sequence is a cDNA encoding novel human protein (NHP) known as human kinase. The human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for

924

840

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Human; kinase polypeptide; PKIN-10; gene therapy; Addison's disease; leukaemia; immune disorder; lymphoma; melanoma; developmental disorder; acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension; asthma; Crohn's disease; rheumacuoid arthritis; bursitis; atherosclerosis; cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer; cholestasis; cardiant; cardiovascular disorder; Niemann-Pick's disease; lipid disorder; fatty liver; daucher's disease; myocardial infarction; drug screening; transgenic animal; antiinflammatory; hepatotropic;
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                                                                                                                            GAGGAAAAGTTCTCAGATGTTCATCCTGTGGCTCTGAACTTCATGAAGGGGGTGTCTGAAG
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Tribouley CM, Bandman O, Nguyen DB, Lu Y, Burford N, Lal P,
Yao MG, Elliott VS, Recipon SA, Kearney L, Lu DAM, Greenwald
Tang YT, Xu Y, Walsh RT, Gietzen KJ, Yang J, Hillman JL;
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239. .1267
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28-JUL-2000; 2000US-022112P.
04-AUG-2000; 2000US-022831P.
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P-PSDB; AAE19152.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       79.1%; Score 823; DB 4; Length 972; 90.6%; Pred. No. 1.7e-209; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 972 BP; 323 A; 172 C; 214 G; 263 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                           therapy for the modulation of NHP expression
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Best Local Similarity 90.6
Matches 929; Conservative
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Ding SR;

treatment of cancer, immune disorder, growth and developmental disorder, cardiovascular disorder and lipid disorder.

Page 183; 196pp; English. Claim 5;

The present invention relates to an isolated human kinase polypeptide (PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is useful for diagnosing, treating and preventing cancer (e.g., leukaemia, I vamphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's disease, rheumatoid arthritis), a growth and developmental disorder (e.g. bursitis, cirrhosis, hepatitis, psoriasis, Cushing's syndrome), a cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial infarction), and a lipid disorder (e.g., fatty liver, cholestasis, Gaucher's disease, Niemann-Pick's disease). PKIN is useful for creating knockin humanised animals or crimine gene therapy, to type. PKIN is useful for creating knockin humanised animals or transgenic animals to model human diseases, in sometic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting calfeferences in the chromosomal location due to translocation, inversion, etc., among normal, carrier or affected individuals, and as hybridisation probes for mapping naturally occurring genomic sequences. PKIN is useful for some or an orther manlysis, dot blot or other membrane-based technologies, in PCR technologies, in pCR technologies, pin will informat enzyme linked immunosorbent (ELISA)-like assays and in microarrays utilising reason teaminance is human bytra.) present sequence is human PKIN-10 cDNA

Sequence 1790 BP; 581 A; 328 C; 366 G; 515 T; 0 U; 0 Other;

Gaps 96; Length 1790; 0; Indels Score 821; DB 6; L Pred. No. 7.4e-209; 0; Mismatches 0; 78.9%; Matches 927; Conservative Local Similarity Query Match

ATGGAAAAGTATGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA 298 1 ATGGAAAAGTATGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA 239 a

> ò 임 ò g ò g ò 유 ò g ò 유 ð 셤

479

CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAAGGAAAATGCATTTAGTTTTT

419

478 300 538 360 598

GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATACAT 301 539

qq 8

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922 840 900 TGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACACTAGTAGAGACG 660 AAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAAGACATGGAAACTCTT 983 GAGGAAAAGTTCTCAGATGTTCATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAG GGGTTTCGCCATGTTGACCAGGCTGGTCTCGAACTCTTGACGTCAAGTGATCCACCTGCC ------AGGAAAATTAATCCCAAGAATCTTT GAGGAAAAGTICTCAGATGTICATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAG 1043 ATGAATCCAGATGACAGATTAACCTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTCT 781 AAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAAGACATGGAAACTCTT ATGAATCCAGATGACAGATTAACCTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTCT 1021 CAG 1023 CAG 1165 923 99 889 841 961 889 901 1163 ઠ 유 ò g ò ద δ g ò 요 ò g 8

ABX08936 standard; cDNA; 1678 BP (first entry) 21-JAN-2003 RESULT 6

cDNA encoding human DITHP protein #6.

Human; ss; gene; diagnostic and therapeutic; DITHP; cancer; arteriosclerosis atherosclerosis; psoriasis; primary thrombocytopenia; autoimmune; inflammatory; anaemia; asthma; autoimmune thyroiditis; crohn's disease; diabetes mellitus; glomerulonephritis; gout; stroke; multiple sclerosis; rheumatoid arthritis; uveitis; AIDS; allergy; acquired immunodeficiency disease; neurological disorder; epilepsy; Alzheimer's disease; dementia; mental retardation; gastrointestinal; Parkinson's disease; ulcer; cirrhosis; reproductive; infertility; endocrine disorder; hyperparathyroidism; hyperlipidemia; hypercholesterolaemia; hypoglycaemia; obesity; Reiter's syndrome; connective tissue disorder; osteoporosis; infection.

Homo sapiens

WO200279473-A2. 10-OCT-2002

658

2001US-0261622P. 2001US-0261864P. 2001US-0261865P. 2001US-0262164P. 2001US-0262164P. 09-JAN-2002; 2002WO-US001009 12-JAN-2001; 16-JAN-2001; 16-JAN-2001; 17-JAN-2001; 17-JAN-2001;

2001US-0262208P. 2001US-0262209P. 2001US-0262215P. 2001US-0263102P 17-JAN-2001; 17-JAN-2001; 18-JAN-2001; 17-JAN-2001;

670

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491 ATAACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAA 550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; protein kinase; PTK; STK; cancer; cardiovascular disease; metabolic disorder; immune related disease; neurological disorder; neurodegenerative disorder; inflammatory disorder; infectious disease; reproductive disorder; gene therapy; ss.
  671 GTTCTTCAGTCGATATATGGGCTATTGGTTGTTTTGCAGAGCTCCTGACAGCCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----AGGAAAATTAATCCCAAGACATCAA
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                                         419 TCAAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGATGCCTACACCGGATT
                                                                                                                                                                                                                                                                                                                                                      479 ATGTAGCTA-CGAGATGGTACCGAGCT-CCTGAACTTCTTGTGGGAGATACT-CAGTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide sequence encoding human protein kinase #25.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention relates to the CDNA and protein sequences of fifty six polynucleotides for diagnostics and therapeutics (DTHP). The human DITHP CC polynucleotides and polypeptides are useful for diagnosing, preventing or treating diseases associated with, as well as effects of exogenous compounds, on the expression of human molecules, such as cell compounds, on the expression of human molecules, such as cell proliferative diseases (e.g. cancer, arteriosclerosis atherosclerosis, proliferative diseases (e.g. cancer), autoimmune/inflammatory diseases (e.g. anaemia, asthm, autoimmune thyroiditis, Crohn's disease, diabetes complitus, glomerulonephritis, gout, multiple sclerosis, rheumatoid arthritis, uveitis, acquired immunodeficiency disease, dementia, arthritis, uveitis, acquired immunodeficiency disease, dementia, neurological disorders (e.g. strock, Alzheimer's disease, dementia, complitues, cirrhosis), reproductive (e.g. infertility, endometriosis), concorring disorders (e.g. hyperparathyroidism, hypercholesterolaemia, hyposlycaemia, hyperlipidemia, obesity), connective tissue disorders (c.g. intergration), practice syndromel, or infertility, endometrion, critical, fungal, paramitic, protozoal). The DITHP sequences may be used to generate hybridisation probes useful in chromosomal mapping of naturally constitue markers, or as antigen to elicit an immune response. The polymucleotides are useful as molecular expressents a human diagnostics and therapeutics (DITHP) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATCCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAAGGAAAATGCATTTAGTTT 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGATCCTGTTGTTAAGAAATAGCACTAAGAGAAATACGTACTGTTGAAGCAATTAAAAC 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                         New human diagnostic and therapeutic (DITHP) polynucleotides and polypeptides, useful for diagnosing, preventing or treating diseases, e.g. cancer, AIDS, Parkinson's disease, or autoimmune/inflammatory
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                                                                                                                                                                                                                                                                                         Jones
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                                                                                                                                                                                                                                                                                    Y, Lincoln SE, Altus CM, Dufour GE, Hillman JL,
Liu TP, Harris B, Plores V, Daffo A, Marwaha R,
Gerstin EH, Peralta CH, David MH, Lewis SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1678 BP; 541 A; 308 C; 336 G; 493 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 267; 331pp; English.
                                         2001US-0262760P.
2001US-0263063P.
2001US-0263064P.
2001US-0263065P.
                                                                                                                                2001US-0263069P.
2001US-0263077P.
2001US-0263329P.
                                                                                                                                                                                                  2001US-0263330P
                                                                                                                                                                                                                                             (INCY-) INCYTE GENOMICS INC.
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19-JAN-2001; 2
19-JAN-2001; 2
19-JAN-2001;
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19-JAN-2001;
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Chang SC,
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Homo sapiens

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421 AAGATTTGTGACTTTGGGGTTTGCAAATTCTGAGTAATTCACATGTTGGGAGAATTGAC 480
361 AACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATC 420
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biological disorder; polymorphism; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS06701-AAS06757 encode for novel human protein kinases #1-57. The novel protein kinases have been identified as members of the tyrosine or scrine/threonine kinase (PTK and STK) families. The polynucleotides encoding protein kinase and the polypeptides may be used in the prevention, diagnosis and treatment of disease associated with impapropriate kinase expression. For example, they may be used to treat cancers (especially cancers of haematopoletic origin), cardiovascular disease (e.g. atheroselerosis), metabolic disorders (e.g. diabetes), immune related diseases (e.g. rheumatoid arthritis), neurological disorders (e.g. disbetes), inflammatory disorders (e.g. asthma), infectious disease (e.g. HIV) and reproductive disorders (e.g. infertility). Additionally, polymucleotides encoding protein kinases may be used for gene therapy and as DNA probes in disponstic assays. The protein kinase polypeptides may be used as antigens in the production of antibodies against the protein kinases and in assays to identify modulators of protein kinase expression and activity
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                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding human kinase polypeptides, useful for preventing diagnosing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections.
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                                                                                                                                                                                                                          Martinez
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                                                                                                                                                                                                                     Sudarsanam S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.7%; Score 757; DB 4; I
86.1%; Pred. No. 7.7e-192;
tive 0; Mismatches 0;
                                                                                                                                                                                                                     Manning G,
                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 1; 433pp; English.
                                                                                         22-NOV-2000; 2000WO-US032085.
                                                                                                                                  24-NOV-1999;. 99US-0167482P
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Matches 927; Conservative
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Clary D;
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                                                                                                                                                                           (SUGE-) SUGEN INC.
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          WO200138503-A2
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Flanagan P,
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CCACTGTGGCCTGGAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACACTAGTA 1097
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                                                                                                                                                                                              618 TCCTTGATTGGCTTAATAGTTGACCTTCTGAATTCTTTTTTCTGCCAATTCAGAGATTTTT 677
                                                                                                                                                                                                                                                               678 CTCCTGGCTTGGATCCATTGCTGACACAGTGTTTCACCATGGGGCCCAGGCTCATCTCGA 737
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                                                                                                                                                                                                                                                                                                                                                                                             798 AGCCACCGTGCCCAGCCAGATTTTTCAAACAATAACTACTGAGAGCTCACAAGATTGTTT 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                  438 GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT 497
                                                                                                                               AAGATTTGTGACTTCGGGTTTGCACAAATTCTGAGTTGGACTTCATCTTTCTCTGGTGCC
                                  AACTGTATTCACAGAGATATAAAACCTGAAAATTATTCTAATAACTAAGCAAGGAATAATC
                                                   GATTATGTAGGTACGAGATGGTACCGAGGTCCTCAACTTCTTGTGGGAGATACTCAGTAT
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                                                                                             421 AAGATTTGTGACTTCGGGTTTGCACAAATTCTG
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                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a novel human protein (NHP) which is a human kinase. A polymorphism was identified in the 3' UTR of the present sequence. The human kinases share structural similarity with animal kinases. More particularly serine or threenine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NMP in the body. The NHP conclocide sequences are useful for generation of antibodies, as reagents products related to human kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or screening disorders. NHP oligonucleotides are used as probes. The labelled NHP probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP products are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
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                                                                                                                                                                                                                                                                           New isolated human kinase polynucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels 306; Gaps
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Pred. No. 6.2e-179;
0; Mismatches 0; Indels 30
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                                                                                                                                                                             Zambrowicz
                                                                                                                                                                             Friedrich G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy for the modulation of NHP expression
                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 34-35; 38pp; English
                                                                                                                                                                           Nehls M,
                                                                              27-SEP-2000; 2000WO-US026621.
                                                                                                              99US-0156511P.
                                                                                                                                             (LEXI-) LEXICON GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 68.1%;
Best Local Similarity 77.0%;
Matches 1025; Conservative (
                                                                                                                                                                             Turner CA,
                                                                                                                                                                                                                             WPI; 2001-266166/27.
P-PSDB; AAE00490.
               WO200123579-A1
                                                                                                              28-SEP-1999;
                                               05-APR-2001
                                                                                                                                                                           Donoho G,
Sands AT;
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654

714

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474

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894

WO2004018641-A2

ADK71927 standard; cDNA; 1266

(first entry) 20-MAY-2004 Human kinase and phosphatase KPP-45 cDNA

hypotensive; vasotropic; antinflammatory; antianginal; anti-HIV; antiallergic; antiaflammatory; antianginal; anti-HIV; antiallergic; antiasthmatic; immunosuppressive; antithyroid; demacological; antidabetic; nephrotropic; antigout; gastrointestinal; neuroprotective; osteopathic; antiarthrilic; uropathic; ophthalmological; antirheumatic; antiparkinsonian; nootropic; anticonvulsant; hepatotropic; antiparaitic; haemostatic; cytostatic; antilipaemic; antiparastic; antihelminic; antibacterial; virucide; protozoacide; fungicide; cardiovascular disease; immune system; neurological; growth; development; cell proliferation; viral; bacterial; fungal; parasitic; protozoan; helminthic infection; transgenic; gene therapy; ss; gene. human; kinase; phosphatase; KPP; cardiovascular; antiarteriosclerotic;

Homo sapiens.

04-MAR-2004

25-AUG-2003; 2003WO-US026635.

26-AUG-2002; 2002US-0406172P. 25-SEP-2002; 2002US-0413910P. 27-SEP-2002; 2002US-0414236F. 11-OCT-2002; 2002US-0417821P.

(INCY-) INCYTE CORP

, Richardson TW, Marquis JP, Swarnakar A, Tang YT; Emerling BM, Jin P, Wilson AD, Yue H, Gietzen KJ; Yang YG, Lee SY, Khare R, Elliott VS, Hafalia AJA; , Ramkumar J, Gururajan R, Tribouley CM, Chien D, Baughn MR,

Tran UK; WPI; 2004-226830/21. P-PSDB; ADK71868. Chawla NK, Murage J;

New human kinases and phosphatases, useful for diagnosing, treating or preventing atherosclerosis, hypertension, AIDS, allergy, multiple sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer or hepatitis.

Claim 5; SEQ ID NO 104; 347pp; English.

kinase and phosphatase (KPP). The polypeptide which is a human kinase and phosphatase (KPP). The polypeptide of the invention demonstrates cardiovascular, antiarteriosclerotic, hypotensiave, vasotropic, antianflammatory, antianginal, anti-HIV, antiallergic, antianflammatory, antianginal, antiallergic, antianflammatory, antison, antianginal, antiallergic, antianterior, antiangentic, antiangentic, antiangentic, antiangentic, antiangentic, antiparkinsonian, nootropic, anticonvulsant, hepatotropic, antipsoriatic, antiparkinsonian, nootropic, anticonvulsant, hepatotropic, antipsoriatic, antipacterial, virucide, protozoacide and fungicide activities. The kinase and phosphatase (KPP) polynucleotides, polypeptides, agonists and antibacterial, virucide, protozoacide and fungicide activities. The kinase and phosphatase (KPP) polynucleotides, polypeptides, agonists and antibacterial, virucide, protozoacide and fungicide activities. The kinase and phosphatase (KPP) polynucleotides, polypeptides, agonists and antibacters may be useful for diagnosing, treating or preventing contents such as cardiovascular diseases, immune system disorders, disorders affecting growth and development, cell glosofers and viral, bacterial, fungal, parasitic, protozoan or helminthic infections. Furthermore, the molecules of the invention may be useful for creating transgenic animals to model human key proma of the invention may be useful for creating transgenic animals to model human key proma of the invention and the proma of the human key proma of the human key proma of the human key proma of the human key control the proma of the human key control of the human key control of the human key control of the human key control of the human key control of the human key control of the human key control of the human key control of the human key control of the human key control of the human key control of the human key control of the human key control of the human key control of the human key control of the human key control of the human key control of KPP CDNA of the invention.

Sequence 1266 BP; 414 A; 234 C; 254 G; 364 T; 0 U; 0 Other;

Query Best Lo Matche	/ Match Local S les 927	67.4%; Score 702; DB 12; Length 1266; imilarity 81.9%; Pred. No. 4e-177; '; Conservative 0; Mismatches 0; Indels 205; Gaps 2;
ò	1	TGGGGT
Db	54	ATGGAAAAGTATGAAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA 113
\$ a	61	TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
ò	121	CCTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACAT 18
qq	174	
٥٧	181	CCAAATCTTGTGAACCTCATCGAGGTGTTTCAGGAGAAAAAGGAAAATGCATTTAGTTTTT 240
Db	234	CAAAT
λo	4	0
DP DP	σ	TGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT 35
රු සි	301	GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
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음 중	361 414	acticiatitacacakatataraaaccigaaaatatrctaatractaatatcaaagaaataatc 420
'n	421	45
qq	474	
ò	455	454
Db	534	TCCTTGATTGGCTTAATAGTTGACCTTCTGAATTCTTTTTTTGCCAATTCAGAGATTTTC 593
λ	455	TTCCAGGAGATGCCTACACCGATTATGTAGCTACGAG 491
Dp	594	9
λ̈́	492	ATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGTTCTTCAGTCGATAT 551
DÞ	654	
ò	552	ATGGCTATTGGTTTTTTTGGAGGTCCTGACAGGCCAGCCA
Dρ	714	Areactalracirerriticadadericreacagecadererergedaa 773
à	612	ATCAGATGTGGACCAACTTTATCTGATAATCAGAACACTAGTAGAGACGGGGTTTCGCCA 671
QQ	774	ATCAGATGTGGACCAACTTTATCTGATAATCAGAACACT
λŏ	672	TGTTGACCAGGCTGGTCTCGAACTCTTGACGTCAAGTGATCCACCTGCCGTAGCCTCTCA 731
Db	813	
λō	732	AAGTGCTGGAATTACAGGAAAATTAATCCCAAGACATCAATCTATTAAAAGTAACGG 791
q 0	813	82
λŏ	792	GITITICCAIGGCAICAGRAIACTGAGCCAGAAGACAIGGAAACTCITGAGGAAAGIT 851
Db	828	91
δλ	N	CTCAGATGTICATCCTGTGGCTCTGAACTTCATGAAGGGTGTCTGAAGATGAATCCAGA 911
qq	918 (zacatgttcatcctgtgggtgaacttcatgaagggggggtgtctgaagatgaat
ολ	912	TGACAGATTAACCIGITCCCAACTCCTGGAGAGCICCTACTTTGATTCTTTTCAAGAGGC 971

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               TGACAGATTAACCTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTCTTTTCAAGAGGC 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated 14257 polypeptide and nucleic acid encoding it. The 14257 protein is a protein kinase that acts as a modulating agent in regulating a variety of cellular processes, including cell proliferation, differentiation, growth and division. The activity of the protein of the invention may be described as, cytostatic, osteopathic; hepatotropic; antidiabetic; neuroprotective; antiarthritic; dermacological; immunosuppressive; antialfammatory; antithyroid; antipporiatic; ophthalmological; antiallergic; antiatchyrimic; antiatherosclerotic; hypotensive; vasotropic; antiarrhythmic; virucide; anorectic; metabolic; immunomodulator and analgesic. The protein of the
                                                                                                                                                                                                                                                     antidiabetic; neuroprotective; antiarthritic; dermatological; immunosuppressive; antiinflammatory; antithyroid; antipsoriatic; ophthalmological; antiallergic; antiathmatic; antiatherosclerotic; hypotensive; vasotropic, antiarthythmic; virucide; anorectic; metabolic; immunomodulator; analgesic; callular proliferative disorder; cancer; acute lymphoblastic leukaemia; Hodgkin's disease; bono metabolism disorder; osteoprorosis; immune system disorder; inflammatory; diabetes mellitus; osteoarthritis; asthma; cardiovascular disorder; hypotension; coronary artery disease; endothelial cell disorder; psoriasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New 14257 polypeptides (protein kinases), useful as diagnostic targets and therapeutic agents for controlling cellular proliferative and/or differentiative disorder, bone disorders, immune disorders and
CCAAATTAAAAGAAAAGCACGTAATGAAGGAAGAAAACAGAAGACGCCAACAG 1023
                                                                                                                                                                                                                                           Protein kinase; enzyme; cytostatic; osteopathic; hepatotropic;
                                                        "Protein kinase 14275"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Fig 1A; 98pp; English
                                                                                                                                   AA164248 standard; cDNA; 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-APR-2001; 2001WO-US012188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-APR-2000; 2000US-0196910P
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129. .815
/*tag= b
/product=
816. .882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                               Human kinase 14257 cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-034355/
P-PSDB; AAG78547.
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                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                       08-MAR-2002
                                        972
                                                                 1038
                                                                                                                                                              AA164248;
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5'UTR
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AAI64248
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invention may act as a novel diagnostic target or therapeutic agent controlling certain disorders, for example kinase-associated or other 14257-associated disorders. These may include cellular proliferative disorders such as cancers e.g. acute lymphoblastic leukemia or Hodgkin's disease. Other disorders include bone metabolism disorders such as osteoporosis, disorders of the immune system, e.g. inflammatory diabetes mellitus, osteoarthritis and asthma. Proteins of the invention may also be of use as therapeutic agents in cardiovascular disorders such as hypertension and coronary artery disease, and some endothalial cell disorders, including psoriasis. The current sequence represents a human kinase 14257 cDNA
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                                                                                                                                                                                                                                                                                                                                   Length 882;
                                                                                                                                                                                                                                                                                        Sequence 882 BP; 288 A; 150 C; 198 G; 245 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                           5; Indels
                                                                                                                                                                                                                                                                                                                                Score 644; DB 6; I
Pred. No. 1.1e-161;
O; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                tch 61.9%;
al Similarity 99.2%;
647; Conservative
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                                                                                                                                                                                                                                                                                                                                Query Match
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Homo

human; kinase and phosphatase; KPP; enzyme; cardiovascular; antiateriosclerotic; hypotensive; vasotropic; antialiflammatory; antianginal; anti-HIV; antiallergic; antiaterhmatic; immunosuppressive; antithyroid; dermatological; antidiabetic; nephrotropic; antigout; gastrointestinal; neuroprotective; osteopathic; antiarthritic; uropathic; ophthalmological; antitheumatic; antipachis; notiarthritic; uropathic; ophthalmological; hepatotropic; (NNS; antipachic; hemostatic; anticornulsant; hepatotropic; (NNS; antipachic; hemostatic; artibacterial; viroide; protozoscaled; fungicide; gene therapy; kinase modulator; phosphatase modulator; cardiovascular disease; immune system disorder; neurological disorder; growth and development disorder; infection; gene; ss.

sapiens

Location/Qualifiers 70. .621

/*tag= a /product= "kinase and phosphatase KPP-41"

WO2004009778-A2

29-JAN-2004

18-JUL-2003; 2003WO-US022650

19-JUL-2002; 2002US-0397354P. 02-AUG-2002; 2002US-0400599P. 02-AUG-2002; 2002US-0400783P. 15-AUG-2002; 2002US-04007PP.

(INCY-) INCYTE CORP

Kable AE, Richardson TW, Becha SD; 3, Lee SY, Griffin JA, Khare R; 8 PR, &warnak A, Chawla NK, Tran UK; 118 JP, Thornton MB, Forsythe IJ, Lee EA; Hafalia AJA, Emerling BM, Kable Al Baughn MR, Tang YT, Lal PG, Lee (Elliott VS, Jin P, Hawkins PR, Sr Gururajan R, Ding L, Marquis JP, Gietzen KJ, Ramkumar J. Baughn MR, Ta Elliott VS, C Gururajan R,

WPI; 2004-132950/13. P-PSDB; ADI40875.

preventing atherosclerosis, hypertension, AIDS, allergy, multiple sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer New human kinases and phosphatases, useful for diagnosing, treating or hepatitis.

Claim 5; SEQ ID NO 94; 330pp; English.

The present sequence encodes a human kinase and phosphatase (KPP)

C protein. KPP sequences have cardiovascular, antiarteriosclerotic,

C hypotensive, vacotropic, antiinflammatory, antianginal, anti-HIV,

antiallerotic, antiathmatic, immunosuppressive, antithyroid,

dermatological, antidiabetic, nephrotropic, anticonvolution that incorportective, osteopathic, nephrotropic, anticonvolution, ophthalmological,

antirheumatic, antiparkinsonian, nootropic, anticonvolusant, hepatotropic,

C antihelmithic, antibacterial, virucide, protozoacide and fungicide

antithelmithic, antibacterial, virucide, protozoacide and fungicide

activities, and can be used in gene therapy, and as kinase modulators and

c antisponists can be used for diagnosing, treating or preventing disorders

C antagonists can be used for diagnosing, treating or preventing disorders

c associated with aberrant expression of KPP, such as cardiovascular

c associated with aberrant expression of KPP, such as cardiovascular

c associated with aberrant expression of KPP, such as cardiovascular

c allergies, asthma, autoimmune thyroiditis, contact dermatitis, angina pectoris

c or congestive heart failure), immune system disorders (e.g. AIDS,

allergies, diabetes mellitus), immune system disorders (e.g. AIDS,

c disease, dabetes mellitus, anulciphe sclerosis, osteoarthritis,

costeoporosis, pancreatitis, Relter's syndrome, rheumatoid arthritis,

c sjogren's syndrome or uveltis), neurological disorders (e.g. Alrheimer's

c places, parkinson's disease, Huntington's disease, dementia or

c places, parkinson's disease, Huntington's disease, dementia or

c places, primary

c thrombocytopenia), cell proliferative disease, psoriasis or primary

c thrombocytopenia), cell proliferative disease, psoriasis or primary

741 909 801

850 acadeceaeceacrerereseaancaeareresaceaeceaecrariareresanaareaea 742 ATTACAGGAAAATTAATCCCAAGACATCAATCAATCTTTAAAAGTAACGGGTTTTTCCAT

682 GCTGGTCTCGAACTCTTGACGTCAAGTGATCCACCTGCCGTAGCCTCTCAAAGTGCTGGA

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120 189 180 369 129 249 240 309 300 360 429 420 489 470 549 609 559 699 729 636 789 681 849 fungal, parasitic, protožoan or helminthic infections. The KPP and polymuclectides are also useful in assessing the effects of exogenous compounds on the expression of nucleic acids and kinases and phosphatases, or for facilitating the drug discovery process, including determination of efficacy, dosage, toxicity and pharmacology. The polymuclectides encoding KPP are useful for creating transgenic animals to model human disease. 70 ATGGAAAAGTATGAAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 490 AAGATTTGTGACTTCGGGTTTGCACAAATTCTGAACACAGTGTTTCACCATGGGGCCCAG 1 ATGGAAAAGTATGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA 121 GATCCTGTTGTTAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACAT 190 GATCCTGTTGTTAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACAT 250 CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAGGAAAATGCATTTAGTTTTT GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT GCTCATCTCGAACTTCTGGCCTCAAGTGATCCTTCCACCTCGGCCTCCCAAAGTGCTGGA 670 CAAGATIGITITIAGIGGAACACAATITICGAACAAATITCITIGAGAACGCATICCAGGAG 181 CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAGGAAAATGCATTTAGTTTTT 370 GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT AAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGATGCCTA-----511 CTTCTTGTGGGAGATACTCAGTATGGTTCTTCAGTCGATATATGGGCTA-----610 Tracaagrereadeceadeceadeceadecaarrrrreaaacaaraacreagagerea 560 --------TIGGITGTGTTTTTGCAGAGCTCTTGACAGGCC --GCCACTGTGGCCTGGAAAATCAGATGTGGACCAACTTTATCTG 730 ATGCCTACACCGATTGTGTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAG ATAATCAGAACACTAGTAGAGACG-------GGGTTTCGCCATGTTGACCAG 790 ATACTCAGTATGGTTCTTCAGTCGATATGGGCTATTGGTTGTGTTTTTGCAGAGCTCCTG --------CACCGATTATGTAGCTACGAGATGGTACCGAGCTCCTGAA Gaps . 66 Length 1429; Sequence 1429 BP; 466 A; 286 C; 294 G; 383 T; 0 U; 0 Other; Indels or cancer), / Match 58.0%; Score 604; DB 12; Local Similarity 75.6%; Pred. No. 6.5e-151; les 848; Conservative 0; Mismatches 175. hypercholesterolaemia, hyperlipidaemia Ä 61 Query Match 301 421 471 550 637 593 Matches 88888888888888 셤 à ò 유 셤 ð 셤 ò q ద ò ò g ò ઠે g ò ద ò q à a ò a

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This invention describes a novel disease detection and treatment molecule polypeptide (MDDT) which has anti-inflammatory, immunosuppressive, cateopathic, cytostatic, anti-inflammatory, immunosuppressive, cateopathic, cytostatic, anti-infly, haemostatic, nephrotropic, cateopathic, cytostatic, anti-inflammatory of anti-inflammatory. The polymeria of the invention can be used for gene therapy, crotein replacement therapy and are useful for treating a variety of diseases or conditions. These polymetides or polymucleotides are particularly useful for diagnosing, treating or preventing cell proliferative disorders (e.g. cancers including adenocarcinoma, cell-enkamia, lymphoma, malanoma, myeloma or sarcoma), anaemia, Crohn's disease, acquired immunodeficiency syndrome (ALDS), Goodpasture's syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or hepatitis. ABX34440-ABX34835 encode the MDDT polypeptides represented in ABU11450-ABU11845, described in the disclosure of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from MIPO at
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 52.2%; Score 543.2; DB 8; Length 1281; Best Local Similarity 99.5%; Pred. No. 1.1e-134; Matches 545; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                               Sequence 1281 BP; 428 A; 191 C; 317 G; 345 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                1030 CATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATTA 1089
                                                      ACCTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTCTTTTCAAGAGGCCCAAATTAAA 1149
                                                                                                          CATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATTA 921
ACACTAGGAAAATTAATCCCAAGACATCAATCAATCTTTAAAAGTAACGGGTTTTTCCAT 969
                                     861
                                                                                                                                                                                  ACCTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTCTTTTCAAGAGGCCCCAAATTAAA 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MDDT; human; disease detection and treatment molecule polypeptide; anti-inflammatory; immunosuppressive; osteopathic; cytoofatic; anti-HIV; haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic; gene therapy; protein replacement therapy; call proliferative disorder; cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; mysloma; sarcoma; anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS; Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New purified disease detection and treatment molecule proteins and polynucleotides, useful for diagnosing, treating or preventing cancers (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis or hepatitis.
                                     GGCATCAGTATACCTGAGCCAGAAGACATGGAAACTCTTGAGGAAAAGTTCTCAGATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 240; 339pp + Sequence Listing; English.
                                                                                                                                                                                                                                                        AGAAAAGCACGTAATGAAGGAAGAACAAAGAGGCCCAACAG 1023
                                                                                                                                                                                                                                                                                          AGAAAAGCACGTAATGAAGGAAGAACAGAAGACGCCAACAG 1191
                                                                                                                                                                                                                                                                                                                                                                                     ABX34679 standard; cDNA; 1281 BP
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2001US-0280067P.
2001US-0280068P.
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2001US-0291829P.
2001US-0291849P.
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2001US-0299776P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human mddt cDNA SEQ ID 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-FEB-2003 (first entry)
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16-MAY-2001;
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17-MAY-2001;
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20-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 AACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATC 420
                            GATCCTGTTGTTAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACAT 180
                                                                                                                                                                                                          883
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                                                                                                                                     764 IGCAGAAACAAAACCICIGGACAAGIAGIAGCIGIIAAAAAAITIGIGGAAICIGAAGAI 823
                                                                                                                                                                                          GTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGGAGATACTCAGTTCT
                                                                                                                                                                                                                                                              181 CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAAAAAGGAAAATGCATTTAGTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGATGCCTACACGATTAT
Gaps
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TACTCAGTATGGTTCTTCAGTCGATATATGGGCTATTGGTTGTTTTTTGCAGAGCTCCT

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Human, mouse, protein kinase, antiarthritic; antisclerotic, osteopathi immunosuppressive, cardiant, renal, antiinflammatory, antiasthmatic, dermacological, antidiabetic; antiinfertility, gene therapy, vaccine, immune disorder; cardiovasease, neurodegenerative disease, cancer; autoimmune disorder; stroke, inflammatory bowel disease, inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
protein kinase cDNA, SEQ ID NO: 49
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sapiens

WO200073469-A2

07-DEC-2000

26-MAY-2000; 2000WO-US014842.

99US-0136503P 28-MAY-1999;

(SUGE-) SUGEN INC.

ŝ Sudersanam Ď, Whyte ď Plowman GD, Martinez

WPI; 2001-032161/04. P-PSDB; AAB65642 Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers.

Example 4; Fig 2; 310pp; English.

The present sequence encodes a novel protein kinase. The nucleic acids and the protein kinases they encode may be used in the treatment and disgusses associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies expression and activity. Diseases related to kinase expression and cartivity. Diseases related to kinase expression and activity include rheumatorid arthritis, atherosclerosis, autoimmune disorders, camplications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative-stress related disorders, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, ostecarthritis, perials, rhinitis, rhinitis, atheometers and reproductive

Sequence 911 BP; 293 A; 182 C; 178 G; 258 T; 0 U; 0 Other;

Ξ, 344 404 120 464 180 524 240 9 285 AAATGGAGTTGCTGATGGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAA 345 ITTCTGTCATATACATAACTGTATTCACAGAGATATAAAAACCTGAAAATATTCTAATAAC 61 TITCIGICATATACATAACIGIATITICACAGAGATATAAAACCIGAAAATATICTAAC 405 TAAGCAAGGAATAATCAAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGA TGCCTACACCGATTATGTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGA Gaps 121 TAAGCAAGGAATAATCAAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGA 96; Length 911; 0; Indels Score 537; DB 4; Pred. No. 4.4e-133; 0; Mismatches Query Match
Best Local Similarity 87.0%;
Matches 643; Conservative 465 181 ò a ò g

New antisense compound targeted to a nucleic acid molecule encoding microtubule-affinity-regulating kinases (MARK3), useful for modulating expression of MARK3 or for treating cancer or Alzheimer's disease.

644 360 764 384 824 504 444 884 944 564 624 AAGACTAGTAGAGACGGGGTTTCGCCATGTTGACCAGGCTGGTCTCGAACTCTTGACGTC GACAGGCCAGCCACTGTGGCCTGGAAAATCAGATGTGGACCCAACTTTATCTGATAATCAG GAAGGGGTGTCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTCCTGGAGAG 505 GAAGGGTGTCTGAAGATGAATCCAGATGACAGTTAACCTGTTCCCAACTCCTGGAGAG 705 AAGTGATCCACCTGCCGTAGCCTCTCAAAGTGCTGGAAATTACAGGAAAATTAATCCCAAG ------AGGAAATTAATCCCAAG 385 ACATCAATCAATCTTTAAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGA 765 ACATCAATCTTTAAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGA 825 AGACATGGAAACTCTTGAGGAAAGTTCTCAGATGTTCATCCTGTGGCTCTGAACTTCAT cancer; MAP/microtubule affinity-regulating kinase 3; c: Alzheimer's disease; neurodegenerative disorde; hyperproliferative disorder; cytostatic. Human; ss; antisense gene therapy; MARK3; 1005 AAACAGAAGACGCCAACAG 1023 643 Human MARK3-associated cDNA #37 Dobie KW; 625 AAACAGAGACGCCAACAG 17-JUN-2002; 2002US-00174319. ADI29367 standard; cDNA; 911 17-JUN-2002; 2002US-00174319 22-APR-2004 (first entry) (ISIS-) ISIS PHARM INC Ward DT, Freier SM, WPI; 2004-052188/05. 361 AACACT--P-PSDB; ADI29249. US2003232771-A1 18-DEC-2003 241 585 301 645 367 885 945 ADI29367; ADI29367 RESULT ద ò ద ò g ò 셤 à a ò 원 셤 ò 셤 ð ò

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625 AAACAGAAGACGCCAACAG 643
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Sands AT;
                                                                                             AAD03812;
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                                                      AAD03812
                                                                                             base pairs (bp) targeted to a nucleic acid encoding MARK3

(MAP/microcubule affinity-regulating kinase 3), that specifically
hybridises with the nucleic acid encoding MARK3 and inhibits expression
of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a
composition comprising the compound and a carrier or diluent, inhibiting
the expression of MARK3 in cells or tissues, treating an animal having or
suspected of having a disease or condition associated with MARK3 and
screening for an antisense compound. The antisense oligonucleotide is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              944
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                           The invention relates to a compound comprising a sequence comprising 8-80
                                                                                                                                                                                                                                                                                                                                                                         404
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                                                                                                                                                                                                                                                                                                                                              1 AAATGGAGTTGCTGATGGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGACATGGAAACTCTTGAGGAAAAGTTCTCAGATGTTCATCCTGTGGCTCTGAACTTCAT
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                                                                                                                                                useful for preparing a composition for treating hyperproliferative disorder, particularly cancer and neurodegenerative disease e.g. Alzheimer's disease. The present sequence is a MARK3 associated CDNA included in the figures but not mentioned anywhere else in the
                                                                                                                                                                                                                                                                                          96; Gaps
                                                                                                                                                                                                                                                           Query Match 51.6%; Score 537; DB 12; Length 911; Best Local Similarity 87.0%; Pred. No. 4.4e-133; Matches 643; Conservative 0; Mismatches 0; Indels 99
                                                                                                                                                                                                                                  Sequence 911 BP; 293 A; 182 C; 178 G; 258 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1005 AAACAGAAGACGCCAACAG 1023.
Disclosure; Fig 2; 233pp, English
                                                                                                                                                                                                           specification.
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The present sequence is a cDNA encoding novel human protein (NHP) known as human kinases. The human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases. Human kinases cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nuclectide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the identification of other cellular gene produces related to human kinases, and as reagents in diagnostic assays, for the identification of other cellular gene produces related to human kinases, and as reagents in diagnostics. NHP oligonucleotides are used as probes. The labelled medical disorders. NHP oligonucleotides are used as probes. The labelled the probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in classocial are used to genetically engineer cells in vivo that functions as body. Nucleotide constructs encoding functional NHPs are used in gene
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/product= "Human kinase #1"
/note= "The coding region does not include stop codon"
/partial
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                                                                                                                                                                                                                                                                                                                    Human; kinase; gene therapy; bioreactor; mental disorder;
biological disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0156511P.
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AAD03812 standard; cDNA; 561
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Matches 455; Conserv
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TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
                                                                                                                     181 CCAAATCTTGTGAACCTCATCGAGGTGTTTCAGGAAAAAAGGAAAATGCATTTAGTTTTT 240
                                                  61 TGCAGAAACAAAACCTCTGGACAAGTAGTTGTAAAAAATTTGTGGAATCTGAAGAT 120
                                                                            121 GATCCTGTTGTTAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACAT 180
                                                                                        301 GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATACAT 360
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AX112442 Ciona int
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Location/Qualifiers

1.1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAT 15-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
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100.0%; Score 1041; DB 6; Length 1041;
Best Local Similarity 100.0%; Pred. No. 2.7e-243;
Matches 1041; Conservative 0; Mismatches 0; Indels 0;
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AR438688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
ACCESSION
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KEYWORDS
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FEATURES Location/Qualifiers 11041 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	Query Match 100.0%; Score 1041; DB 6; Length 1041; Best Local Similarity 100.0%; Pred. No. 2.7e-243; Matches 1041; Conservative 0; Mismatches 0; Indels 0; Gaps (QY 1 ATGGAAAAGTATGAAAAATTAGCTAAGACTGAGAAGGGTCTTATGGGGTTGTATTCAAA 60 DD 1 ATGGAAAAGTATGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA 60	QY 61 TGCAGAAACAAAACCCTGGACAAGTAGCTGTTAAAAAAATTTGTGGAATCTGAAGAT 120 Db 61 TGCAGAAACAAAACCCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120	QY 121 GATCCTGTTGTTAAGAAAATAGCACTAAGAAATACGTATGTTGAAGCAATTAAAACAT 180 Db 121 GATCCTGTTGTTAAGAAAATAGCACTAAGAAAATACGTATGTTGAAGCAATTAAAACAT 180	OY 181 CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAGGAAAATGCATTTAGTTTTT 24C	QY 241 GAATACHGIGATCATACACTITITAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT 300 DD 241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAA	Qy 301 GGAGTGATCAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360	QY 361 AACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATC 420 DD 361 AACTGTATTCACAGAGATATAAAACCTGAAAAATATTCTAATAACTAAGCAAGGAATAATC 420	Oy 421 AAGATITGTGACTITGGGGTTTGCACAAATTCTGATTCCAGGAGATGCCTACACCGATTAT 480 Db 421 AAGATITGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGATGCCTACACCGATTAT 480	Qy 481 GTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGTTCT 540	Oy 541 TCAGTCGATATATGGGCTATTGGTTGTGTTTTTGCAGAGCTCCTGACAGGCCAGCCA	Qy 601 TGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACACTAGTAGAGACG 660 	QY 661 GGGTTTCGCCATGTTGACCAGGCTGGTCTCGAACTCTTGACGTCAAGTGATCCACCTGCC 720 DD 661 GGGTTTCGCCATGTTGACCAGGCTGGTCTCGAACTCTTGACGTCAAGTGATCCACCTGCC 720	721 GTAGCCTCTCAAAGTGCTGGAATTACAGGAAAATTAATCCCAAGACATCAATCA	DD /21 GIAGCCICICARAGIGCIGGARATTACAGGARAATTAATCCCAAGACATCAATCAATCTT 780 781 AAAAGTAACGGGTTTTTTCCATGGCAATCAGTATACCTGAGGCGAGAAGACATGGAAACTTTTTTCATGGCATATAACTGAGGCGAGAAGACATGGAAACTTTTTTTT	Db 781 AAAGTAACGGGTTTTCCATGGCATCAGTATACCTGAGCCAGAAGACATGGAAGTCTT 840	QY 841 GAGGAAAGTTCTCAGATGTTCATCCTGTGGCTCTGAACTTCATGAAGGGGGTGTCTGAAG 900	901 ATGAATCCAGATGACAGATTAACCTGTTCCCAACTCCTGGAGGCTCCTACTTTGATTCT
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		Oy 1021 CAGGT 1025 Db 1021 CAGGT 1025		REFERENCE 1 AUTHORS Donoho,G., Turner,C.A., Nehls,M., Friedrich,G., Zambrowicz,B. and Sands,A.T. TITLE Human kinase proteins and polynucleotides encoding the same JOURNAL Patent: WO 0123579-A 3 05-APR-2001; Lexicon Genetics Incorporated (US) FEATURES Location/Qualifiers Source /organism="Homo sapiens" //mol_type="unassigned DNA" //db_xref="taxon:9606"	Query Match 98.5%; Score 1025; DB 6; Length 1068; Best Local Similarity 100.0%; Pred. No. 2.2e-239; Matches 1025; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Oy 1 AIGGAAAAGIAIGAAAAAITAGCIAAGACIGGAGAAGGGICTIAIGGGGIIGIAITCAAA 60		Qy 121 GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACAT 180
Db 901 ATGAATCCAGATGACAGATTAACCTGTTCCCAACTCCTGGAGGCTCCTACTTTGATTCT 960 Qy 961 TTTCAAGAGGCCCAAATTAAAAGAAAAGCACGTAATGAAGGAAG	RESULT 3 AR492166 LOCUS LOCUS AR492166 LOCUS AR492166 DEFINITION Sequence 3 from patent US 6716616. ACCESSION AR492166 A	Query Match 98.5%; Score 1025; DB 6; Length 1068; Best Local Similarity 100.0%; Pred. No. 2.2e-239; Matches 1025; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY 1 ATGGAAAAGTATGAAAATTAGCTAAGACTGGAGAAGGTCTTATGGGGTTGTATTCAAA 60 Db 1 ATGGAAAAGTATGAAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA 60 QY 61 TGCAGAAACAAAAACTCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120 Db 61 TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAAATTGTGGAATCTGAAGAT 120 QY 121 GATCCTGTTGTTAAGAAATAGCACTAAGAGAAATACGTATGAAGCAATTAAAACAT 180 Db 121 GATCCTGTTGTTAAGAAATAGCACTAAGAGAAATACGTATGATGAAGCAATTAAAACAT 180	Qy 181 CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAGGAAAATGCATTTAGTTTTT 240 Db 181 CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGGAAAAAGGAAATGCATTTAGTTTTT 240 Qy 241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAA	OY 361 AACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGGAAGG	OY 421 AAGATITGIGACTICGGGTTIGCACAAATICTGATICCAAGAGATGCCTACACCGATTAT 480 DD 421 AAGATITGIGACTICGGGTTIGCACAAATICTGATICCAAGAGATGCCTACACCGATTAT 480	OY 481 GTAGCTACGAGATGGTACCGAGGTCCTGAACTTCTTGTGGGGADACTCAGTATGGTTCT 540	Qy 541 TCAGTCGATATATGGGCTATTGGTTTTTTTGCAGAGCTCCTGACAGGCCAGCCA

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Donoho, G., Turner, C.A. Jr., Nehls, M.C., Friedrich, G., Zambrc and Sands, A.T.
Human Kinase proteins and polymucleotides encoding the same Patent: US 6716616-A 11 06-APR-2004;
Location/Qualifiers
1 945
/ organism="unknown"
/ mol_type="genomic DNA" 96; Length 945; Indels Score 839; DB 6; L Pred. No. 5.1e-194; 0; Mismatches 0; 80.6%; al Similarity 90.8%; 945; Conservative Unclassified Query Match Best Local (121 241 301 301 361 421 421 481 481 541 601 601 661 651 721 651 841 Best Loca Matches TITLE JOURNAL FEATURES REFERENCE AUTHORS qq ò g ò 원 à

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DNA

AR492170 945 bp Sequence 11 from patent US 6716616. AR492170.1 GI:47260680

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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 5 AR492170 LOCUS

DD 421 AAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGATGCCTACACGGTTAT 480	OY 481 GTAGGTACGAGATGCTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCGTATGGTTCT 540	OY 541 TCAGTGGATATATGGGCTATTGGTTTTTTGCAGAGCTCCTGACAGCCAGC	Oy 601 TGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACACTAGTAGAGCG 660 	GGGTTTCGCCATGTTGACCAGGCTGGTCTCGAACTCTTGACGTCAAGTGATCCACCTGCC	ON 721 GTAGCCTCTCAAAGTGCTGGAATTACAGGAAAATTAATCCCAAGACATCAATCA	781 AAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAAGACATGAACTCTT		Qy 841 GAGGAAAGTICTCAGAIGTICATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAG 900	OY 901 AIGAAICCAGAIGACAGAITAACCIGIICCCAACICCIGGAGAGCICCIACTITGAITCT 960	OY 961 TITCAAGAGGCCCAAATTAAAAGAAAAGGACACGTAATGAAGGAAG	Qy 1021 CAGGTACTTCCGCTCAAAGT 1041 	AR492167	TION Sequence S ION AR492167 N AR492167.1 DS	972)	and Hum Pat	ource	atch 79.1%; Score 823; DB 6; Length 972; cal Similarity 90.6%; Pred. No. 4.1e-190;	17AG
Db 745 GAGGAAAAGTTCTCAGATGTTCATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAG 804	Oy 901 ATGAATCCAGATGACAGATTAACCTGTTCCCAACTCCTGGAGGCTCCTACTTTGATTCT 960	OY 961 TITCAAGAGGCCCAAATTAAAGAAAAGCACGTAATGAAGGAAG	Qy 1021 CAGGTACTTCCGGTCAAAAGT 1041 Db 925 CAGGTACTTCCGCTCAAAAGT 945	RESULT 6	AALO/122 ALOCUS DEFINITION Sequence 11 from Patent W00123579. ACCESSION AX107722 ACCESSION AX107722	S	OKGANISM Homo Baptens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primetes; Catarrhini; Hominidae; Homo.	<pre>CE 1 RS Donoho,G., Turner,C.A., Nehls,M., Friedrich,G., Zambrowic Sands,A.T.</pre>	JILLE Human Klidase proteins and polynucieotides encoding the same JOURNAL Patent: WO 0123579-A 11 05-APR-2001; Lexicon Genetics Incorporated (US) FEATURES Location/Qualifiers	ource	ORIGIN Query Match Best Local Similarity 90.8%; Pred. No. 5.1e-194; Matches 945; Conservative 0; Mismatches 0; Indels 96; Gaps 1;	Oy 1 ATGGAAAAGTATGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA 60 	Qy 61 TGCAGAAACAAACCTCTGGACAAGTAGTAGTAGCTGTTAAAAATTTGTGGAATCTGAAGAT 120 Db 61 TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120	Qy 121 GATCCTGTTGTTAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACAT 180	Qy 181 CCAAATCTTGTGAACCTCATCGAGGTTTCAGGAGAAAAAGGAAATGCATTTAGTTTTT 240 Db 181 CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAAGGAAAATGCATTTAGTTTTT 240	Qy 241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGAACCCAAATGGAGTTGCTGAT 300	Qy 301 GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATACAT 360	Qy 361 AACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGGAATAATC 420

1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Oy 181 CCAA Oy 181 CCAA Oy 241 GAA1 Ob 241 GAA1 Oy 301 GGAG Oy 361 AACT Oy 361 AACT Oy 421 AAGA Oy 481 GTAG Oy 481 GTAG Oy 601 TGGC Oy 601 TGCC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGCC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGCC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGCC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601 TGGC Oy 601
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alla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ds,A.T.
an kinase proteins and polynucleotides encoding the same
ant: WO 0123579-A 5 05-APR-2001;
icon Genetics Incorporated (US)
Location/Qualifiers
1. 972
/organism="Homo sapiens"
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larity 90.6%; Pred. No. 4.1e-190;
Conservative 0; Mismatches 0;
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QY 241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGCAACCCAAATGGAGTTGCTGAT 300 Db 479 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGCAAATGGAGTTGCTGAT 538 QY 301 GGAGTGATCAAAAGCGTATTTAAATGAGCACTTCAAGCTCTTAATTTCTGTCATATACAT 360 Db 539 GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT 598 QY 361 AACTGTATTCACAGAGATATAAAACCTGAAAATTTCTAATAATTTCTGTCATATACAT 598 QY 421 AAGATTTGTGACTACAGGATATAAAACCTGAAAATTTCTAATAACTAAGCAAGGAATAATC 658 QY 421 AAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGGAATAATC 718 QY 421 AAGATTTGTGACTTCGGGTTTGCACAAATTCTTGATTACCAGGAGTGCCTACACCGATTAT 718 QY 421 AAGATTTGTGACTTCGGGTTTGCACAAATTCTTGTGAGGAATACTCTGTTTTTTTT	00 TGGCCTGGAAATCAGATGTGCACCAACTTTATCTGATAATCAGAACATGTAGAGACG 660	AX698820 LOCUS LOCUS Sequence 6 from Patent W002079473. AX698820 VERSION AX698820 VERSION AX698820 VERSION AX698820 VERSION AX698820 VERSION AX698820 VERSION AX698820 VERSION AX698820 VERSION AX698820 VERSION AX698820 VERSION AX698820 VERSION AX698820 VERSION AX698820 VERSION AX698820 VERSION AX698820 VERSION FORCE Nome sapiens Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo. AUTHORS Panzer, S.R., Lincoln, S.E., Altus, C.M., Dufour, G.E., Hillman, J.L., Jones, A.L., Dam, T.C., Liu, T.F., Harris, B., Flores, V., Daffeo, A., Marwaha, R., Chen, A.J., Chang, S.C., Gerstin, J.E., Peralta, C.H., David, M.H. and Lewis, S.A.
	RESULT 9 AX746179 AX746179 AX746179 AX746179 AX746179 AX746179 AX746179 AX746179 AX746179 AX746179 AX746179 AX746179 AX746179.1 AX74	Qy 1 ATGGAAAAGTATGAAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA 60 Db 239 ATGGAAAAGTATGAAAAATTAGCTAAGACTGGAAAGGGTCTTATGGGGTTGTATTCAAA 298 Qy 61 TGCAGAAACAAAACTCTGGACAAGTAGTAGTAGAAAATTTGTGGAATCTGAAGAT 120 Db 299 TGCAGAAACAAAACACTCTGGACAAGTAGTAGTGTTAAAAAATTTGTGGAATCTGAAGAT 358 Qy 121 GATCCTGTTGTTAAGAAATAGCACTAAGAGAAATAGGTGTTGAAGCATTAAAACAT 180 Db 359 GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAATAGGTGTTGAAGCATTAAAACAT 418 Oy 1181 CCAAATCTTGTGAACCTCATGGGGTGTTCAGGAGAAAAGGAAAAGGAAAATGATTTT 240 Db 419 CCAAATCTTGTGAACCTATCATGAGGAAAAAGGAAAAAGGAAAATGCATTAAGTTTT 478

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72.7%; Score 757; DB 6; I. 86.1%; Pred. No. 5.1e-174; ative 0; Mismatches 0;
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    .1083
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Sequence 25 from Patent W00138503.
AX166534
AX166534.1 GI:14546879
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Best Local Similarity 86.1
Matches 927; Conservative
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                                                                                                       Query Match
73.3%; Score 762.8; DB 6; Length 1678;
Best Local Similarity 90.0%; Pred. No. 2e-175;
Matches 925; Conservative 0; Mismatches 2; Indels 101;
                                     1. 1678 | forganism="Homo sapiens" | forganism="Homo sapiens" | forganism="Laxon: 5606" | forganism="Incyte ID No: LI:058298.1:2001JAN12"
Molecules for diagnostics and therapeutics
Patent: WO 02079473-A 6 10-OCT-2002;
Incyte Genomics, Inc. (US)
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Plowman, G.D., Whyte, D., Manning, G.S., Sudarsanam, S.S., Martinez, R., Flanagan, P. and Clary, D.S.
Novel human protein kinases and protein kinase-like enzymes
Patent: WO 0138503-A 25 31-MAY-2001;
Sugen, Inc. (US)
Location/Qualifiers CTCTTGAGGAAAAGTTCTCAGATGTTCATCCTGTGGCTCTGAACTTCATGAAGGGGTGTC 934 PAT 22-JUN-2001 120 61 TGCAGAAACAAAACCTCTGGACAAGTAGTGGTTAAAAAATTTGTGGAATCTGAAGAT 120 180 180 240 240 Homo sapiens Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 300 300 360 420 454 9 9 1 ATGGAAAAGTATGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA 61 TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAATTTTGTGGAATCTGAAGAT GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACAT ACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATC CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAAGGAAAATGCATTTAGTTTTT GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT AACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATC 150; Length 1083; Indels

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421 AAGATITGTGACTTCGGGTTTGCACAATTCTGAGTAATTCACATGTTGGGAGAATTGAC 480 455TTCCAGGAGATGCCTACACGAGTATTGTGAC 486 481 TTACCTGATCGATTGATGCATTTGCAGTTGCGAGATGCCTACACGATTATGTAGCT 540 487 ACGAGATGCGACTCCTGAACTTCTTGTGGAGATGCCTACAGTTATGTTCGTC 540		727 TCTCAAAGTGCTGGAATTACAGGAAATTAATCCCAAGACATCAATCTATAAAGT 786	AAGTICTCAGATGTTCATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGAGTGAAT 	CCAGATGACAGATTAACCTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTCTTTCT	967 GAGGCCCAATTAAAAGAAAGCACGTAATGAAGGAACAAACA	RESULT 12 . AR492171 LOCUS AR492171 1819 bp DNA linear PAT 15-MAY-2004 DEFINITION Sequence 13 from patent US 6716616. ACCESSION AR492171. KEYWORDS .	SOURCE Unknown. ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 1819)	and Sands, A.T. Human kinase proteins and polynucleotides encoding the Patent: US 6716616-A 13 06-APR-2004; Location/Qualifiers	rce	y Match 68.1%; Score 709; DB 6; Length 1819; Local Similarity 77.0%; Pred. No. 2.6e-162;	Tractantenes of incers 505 caps Tractantenes of incers 505 caps	138 ATGGAAAAGTATGAAAAATTAGCTAAGACTGGAGAAAGGGTCTTATGGGGTTGTACAAA 197 61 TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120

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Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                         Length 687;
                 Kapeller-Libermann, R.
14557, protein kinase molecules and uses therefor Patent: WO 0179488-A 3 25-OCT-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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Pred. No. 7.7e-147;
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Local Similarity 99.4%;
Hes 648; Conservative 0
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                 14257, protein Kinase molecules and uses
Patent: WO 0179488-A 1 25-OCT-2001;
Millennium Pharmaceuticals, Inc. (US)
1. .882
Kapeller-Libermann, R.
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Search completed: April 21, 2005, 23:37:10 Job time : 4539.25 secs

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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to
          Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,T., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the Mouse transcriptome based on functional annotation of 60,770 full.length cDNAs
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The Institute of Physical and Chemical Research (RIKEN)
1-22 Subehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
Fax: 81-45-503-9216
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Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Yukuda,S., Hashizume,W., Hayashida,K., Hizozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsaco,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Direct Submission
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Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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/clone="G630052E12"
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BY733578 RIKEN full-length enriched, 16 days neonate male diencephalon Mus musculus CDNA clone G630052E12 5', mENA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Fukunishi, Y., Hara, A., Hayatau, N., Hiramoco, K., Hiramoco, K., Hiramoco, K., Hiramoco, K., Inchi, M., Itahi, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Koula, M., Izawa, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Salto, R., Sakai, C., Sakai, Y., Suno, H., Sasaki, D., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Voshino, M., Muramatsu, M. and Hayashizaki, Y. Tona, T., Direct Submission

Li Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Styloration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, Tg-22, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-9222, 1-4-5-61-921-9222, 1-4-5-61-921-9222, 1-4-5-61-921-9222, 1-4-5-61-921-
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KRAIARBIRALKQLKHPNIVNLLEVERKRRHLIPUFENDHTVHELDRYGKGVBED-
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BOLIPRHQOVFSNMQYFSGVKIPDPEDMETLELKFPNISYSALGFLKGCLHMDPAERL
TCEQLLQHPYFDSIRGGLTRQHDKPARKTLRQSRKHLTGLQYLPGLTSSRILPALD
NKKXHGSTKRFNYHFPNI"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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transcriptome based on functional annotation
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kinase-like 1 (CDC2-related kinase) (MGD|MGI:1918341)
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/clone="4933411017"
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/db_xref="G1:26382418"
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/strain="C57BL/6J"
                                                         Nature 420, 563-573 (2002)
6 (bases 1 to 1691)
Adachi,J., Aizawa,K., Akah
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full-length
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Best Local Similarity 66.9
Matches 587; Conservative
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                                                                                                                                                               GAGTACTGTGATCACACACTGTTAAACGAGCTGGAGAGAAAAACCCAAACGGAGTTTCTGAT 444
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                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4933411017 product:cyclin-dependent kinase-like 1 (CDC2-related kinase), full insert sequence.
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                                                                                                                         Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTAGCTACGAGATACCGAGCTCCTGAACTTCTTGTGGGAGATA 526
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High efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
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Tumor Gene Index

Unpublished (1997)

Context: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: John C. Marshall, M.D., Ph.D

Emails: cgapbs-r@mail.nih.gov

Tissue Procurement: John C. Marshall, M.D., Ph.D

CDNA Library Preparation: CLONTECH

CDNA Library Prayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: NUI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov

Plate: LLCM3144 row: i column: 16

High quality sequence stop: 468.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            721 GAGCCAGAAGACATGGAAACTCTTGAGGAAAAGTTCTCAGATGTTCATCCTGTGGCTCTG 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Globellbe-NUICHD Rr Pitl"
//note="Vector: pDNR-LIB; Site 1: Sfil; Site 2: Sfil; 5' and 3' adaptors were used in Cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CATCTAGAGGCGGGGGCGACATG-GT[30] BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.23 kb (range 0.5-4,0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
     1 (bases 1 to 825)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216 erreccaccaderecradececercaacricirerecaacacacaacaacaaceece
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Rattus norvegicus"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:6888377"
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AGENCOURT 11526413 NICHD Rr Pit1 Rattus norvegicus cDNA clone
IMAGE:6888377 5', mRNA sequence.
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                                                                                                                                                                                                                GACCCTGTCATAAAGAAAATGGCCCTTCGAGAAATCCGCATGCTCAAGCAACTCAAGCAC 356
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Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.
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CTGTTGCAGCATCCATATTTTGACAGCATTCGAGAAG 1053
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CB315094.1 GI:28838974
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VERSION KEYWORDS SOURCE ORGANISM ACCESSION

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BESTIONS (Note mouse)

Mus musculus (house mouse)

Mus musculus

Bukaryota; Marazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Musmania; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 689)

SS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,

Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,

Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,

Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,

Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matuda,H.,

Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,

Chothia,C., Corbani,L.B., Cousling,S., Dalla,E., Dragani,T.A.,

Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,

Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,

Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,

Maltais,L., Marchionni,L., McKenzie,L., Mixi,H., Nagashima,T.,

Numaca,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,

Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,

Ravasi,T., Red,J.C., Reed,D.C., Reid,J., Ring,B.Z., Kingwald,M.,

Sandelin,A., Schneider,C., Semple,C.A., Setcu,M., Shimada,K.,

Wangi,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,

Hayzeuch,N., Harozane-Kishikawa,T., Konno,H., Nakamura,M.,

Sakatume,N., Sato,K., Shirahi,T., Waki,K., Kawai,J., Alzawa,K.,

Kakawa,T., Pukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,

Rogers,J., Birney,B. and Hayashizaki,Y.

Rogers,J., Birney,B. and Hayashizaki,Y.

Analysis of the mouse transcriptome based on functional annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY752739 RIKEN full-length enriched, adult inner ear Mus musculus CDNA clone F930014106 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                416 TGGCATCAGTATACCTGAGCCAGAAGACATGGGAAAAGTTCTCAGATGT 357
                                                                                                                                       536 GACAGGCCACTGTGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAG 477
                                                                                                                                                                                                                                               476 AACACTAGGAAATTAATCCCAAGACATCAATCAATCTTTAAAAGTAACGGGTTTTTCCA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                           356 TCATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          825 AACCTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTCTTTTCAAGAGGCCCAAATTAA 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   885 AAGAAAAGCACGTAATGAAGGAAGAAACAGAAGACGCCAACAGGTACTTCCGCTCAAAAG 944
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                                                                                                                                                                                                                                                                                                       TGGCATCAGTATACCTGAGCCAGAAGACATGGAAACTCCTTGAGGAAAAGTTCTCAGATGT
                                                                                                                                                                                                                                                                                                                                                                                                               TCATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATT
     Pred. No. 5.5e-81;
0; Mismatches 0; Indels
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        100.08;
  Local Similarity 100.
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                                                                                                                                                                                                                                                                        BU686325
UI-CF-DU1-adn-i-10-0-UI.81 UI-CF-DU1 Homo sapiens CDNA clone
UI-CF-DU1-adn-i-10-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mmx".
/mol_type="mxxx".
/mol_type="mxxx".
/mol_type="mxxx".
/clone="ur-cF-0U1-adn-i-10-0-UI"
/tissue_type="primary Lung Epithelial Cells"
/dev stage="Adult"
/lab_host="bH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="ul-CF-0U1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Iowa
2024 University of Iowa
Tel: 319 356 4866
Fax: 319 356 4866
Fax: 319 356 4866
Fax: 319 and-mccray@niowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
Eukaryogisti, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 536)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.2%; Score 361; DB 5; Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (www.openbiosystems.com)
Seg primer: M13 FORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                BU686325.1 GI:23541120
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: McCray, PB
                                                                                    900 TGAAGG 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                    636 TGAGGG 641
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AUTHORS
TITLE
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PEATURES

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m134h09.yl Stratagene mouse testis (#937308) Mus musculus cDNA
clone IMAGE:513953 5' similar to gb:X66358 SERINE/THREONINE-PROTEIN
KINASE KKIALRE (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 27-JAN-1999
                                                409 GAGTACTGTGATCACACGCTGTTAAACGAGCTGGAGAGAAACCCAAACGGAGTTTCTGAT 468
                                                                                                                                        GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAAATTTCTGTCATATACAT 360
                                                                                                                                                                                                                                                                AACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGGAATAATC 420
            529 AATTGTATTCATCGGGATGTAAAACCTGAAAACATCCTAATAACCAAGCAGGGGTGANT 588
                                                                                                                                                                                                                                                                                                                                                                                     AAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGATGCCTACACGGATTAT 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     589 AAGATTTGTGACTTTGGATTTGCACGAATTCTAATTNCA-GAGACGCCTACACANGACTA 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muzidae; Muzinae; Mus.
1 (Dases 1 to 500)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Puderwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Swaller,T., Gibbons,M., Pepc,D., Harvey,M., Schurk,R.,
Ritter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
The WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Stratagene mouse testis (#937308)"
/note="Organ: testis; Vector: pBluescript SK-; Site_l:
EcoR]; Site_2: Xhol; Cloned unidirectionally. Primer:
Oligo dT. Average insert size: 1.0 kb; Uni-ZAP XR Vector;
-5 adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                  469 GGAGTGATTAAAAGTGTGTGTATGGCAAACCCTTCAAGCCCTTAACTTCTGTCAAGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue type="testis"
dev stage="10-12 week old"
lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 GTAGCTACGAGATGGTACCGAGCTCCTGA 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    648 TGTGCCANCCAGTGGTACCGAGCCCCCGA 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   500 bp
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Location/Qualifiers
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'clone="IMAGE:513953"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
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/strain="CD-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                     Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Mormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) RIKBN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKBN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prepare mouse tissues.

Tissues were provided by Kirk W. Beisel ( Boys Town National Research Hospital 555 North 30th Street Omaha,NE 68131 USA ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                       Email: genome_resegsc.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,M., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kwai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M., and Hayashizaki,Y.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229 TGCAGAAACAAATCTTCTGGACAAGTAGTAGCGATCAAAAATTCGTGGAATCTGAAGAT 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GATCCTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACAT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTATGGGGTTGTATTCAAA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAAGGAAAATGCATTTAGTTTTT
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/strain="C57BL/6J"
/db.xref="taxon:10090".
/clone="F930014106"
/tissue type="inner ear"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
                                                                                                                        Contact: Yoshihide Hayashizaki
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60,770 full-length cDNAs
                                   Nature 420, 563-573 (2002)
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organism="Gallus gallus"
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Best Local Similarity 67.2
Matches 483; Conservative
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603750354F1 CSEQCHNO4 Gallus gallus cDNA clone ChEST661113 5', πRNA
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                                                                                                                                                                                                                                                                        179 TGTGCTATGGCAAACCCTTCAAGCCCTTAACTTCTGTCACAAGCACAATTGTATTCATCG 238
                                                                                                                                                                                                                                                                                                                                                                       435 CGGGTTTGCACAAATTCTGATTCCAGGAGATGCCTACACCGATTATGTAGCTACGAGATG 494
                                                                                                                                                                                                                                                                                                                                                                                      299 TGGATTTGCACGAGTTCTAATTCCAGGAGACGCCTACACACAAGTTGCCACCAGCAGGTG 358
                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACATCCAAATCTTGTGAA 194
                                                                                                                                                                                                  255 TACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGATGGAGTGAAAAG 314
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                                                                                                                                          CCTCATCGAGGTGTTCAGGAGAAAAGGAAAATGCATTTTAGATTTTTGAATACTGTGATCA 254
                                                                                                                                                                                                                                                                                                                                                                                                                               GTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGTTCTTCAGTCGATATATG 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAAATAGCCCTGCGCGAAATCCGTATGCTGAAG---TTGAAACACCCCAAACCTCGTGAA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 824)
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                                                                                                                                                          239 GGATGTAAAACCTGAAAACATCCTAATAACCAAGCAAGGGATGATAAAGATTTGTGACTT
                                                                                                                                                                                                                                                       CGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACATAACTGTATTCACAG
                                                                                                                                                                                                                                                                                                               375 AGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATCAAGATTTGTGACTT
                                                         Gaps
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                                                     . 4 ;
                             DB 1; Length 500;
                          Score 333.6; DB 1; Length
Pred. No. 5.3e-74;
0; Mismatches 84; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: Simon. Hubbard@umist.ac.uk.
Location/Qualifiers
1. .824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BU221831.1 GI:25410266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             615 AGATGTGGACCAACTT 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGACGTGGACCACCTT 493
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                          Query Match 35.3%;
Best Local Similarity 82.3%;
Matches 408; Conservative
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Fax: 01612360409
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KEYWORDS
SOURCE
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AUTHORS
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/tissue_type="whole embryo"
/dev_stage="20-21"
/lab.host="Bhlob"
/lab.host="Bhlob"
/clome lib="CSEQCHN4"
/note="Organ: whole embryo; Vector: pBluescript II KS(+);
Site.l: ECGRI; Site.2: Noti; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand synthesis reaction.
Following this first strand synthesis reaction.
Following this first strand caction, double-stranded cDNA
was blunted, ligated to Not! adapters, digested with
ECGRI, size-selected, and cloned into the Not! and ECGRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9212 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 ATGTTGAAGCAATTAAAACATCCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 ATGCTGAAGCAACTGAAAACCCCCAACCTGGTGAACCTGCTGGAGGTGTTCAGGAGAAAG 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280 AACCCAAATGGAGTTGCTGATGGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCT 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         340 CITAATITICIGICATATACATAACIGIATITCACAGAGATATAAAACCIGAAAATATICTA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 GTGAACTTTTGTCACAAACACAACTGCATCCATCGAGATGTAAAGCCAGAAAACATCCTG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATAACTAAGCAAGGAATAATCAAGATTTGTGACTTCGGGTTTGCACAAATTCTGATT--- 456
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/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/dD_xref="taxon:9031"
/clone="ChEST661113"
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m134h09.rl Stratagene mouse testis (#937308) Mus musculus cDNA
clone IMAGE:513953 5' similar to gb:X66358 SERINE/THREONINE-PROTEIN
KINASE KKIALRE (HUMAN);, mRNA sequence.
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                      223 GACCCTGTCATAAAGAAATCGCCCTTCGAGAAATCCGCATGCTCAAGCAACTCAAGCAT 282
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                             301 GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT
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                                                                                    CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAGGAAAATGCATTTAGTTTTT
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Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashI-HHMI Mouse EST Project
Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: mouseest@watson.wustl.edu
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High quality sequence stop: 442.
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/mol_type="mRNA"
/strain="CD-1"
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/note="Organ: kidney; Vector: pExpress-1; Site_1: EcoRV;
Site_2: Not1; RNA obtained from pooled kidney tissue from a mix of male and female animals at 8 wk old. Tissues were snap-frozen before RNA extraction and purification
(Tri-reagent method). CDNA was primed using oligo-dr primer: 5'-pGACTNGTTCTNGATCGCGAGCGCCGCCCT)25-3' and cloned into the EcoRV/NotI sites of pExpress-1.
Size-selection 2.4kb resulted in an average insert size
                                                                                                                                                                                                                                       CK482747

AGENCOURT 17606510 NIH MGC 235 Rattus norvegicus cDNA clone IMAGE:7110321 5', mRNA sequence.
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              753
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Daniela S. Gerhard, Ph.D.

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rml0A07 Betheada, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Howard Jacobs

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.linl.gov e column: 07
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695 GGTTTTTCCATGGCATCAGTATACCTGAGCCAGAAGACATGGAAACTCTTGAGGAAAAG
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 1.1e-69;
0; Mismatches 182;
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/db_xref="taxon:10116"
/clone="IMAGE:7110321"
/tissue_type="kidney, pooled"
/lab_host="DH10B TonA"
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this is a NIH_MGC library."
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Location/Qualifiers
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Rattus norvegicus
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Matches 439; Conservative (
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Matches 42
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Primer:
XR Vector;
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                                                                                                                                                                                                                                                                                                                                                CACACTGTTAAACGAGCTGGAGAGAAACCCAAACGGAGTTTCTGATGGAGTGATTAAAAG 177
                                                                                                                                                                                                                                                                                                                                                                                                 178 TGTGCTATGGCAAACCCTTCAAGCCCTTAACTTCTGTCACAAGCACAATTGTATTCATCG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                297
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                                                                                                                       adaptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          435 CGGGTTTGCACAAATTCTGATTCCAGGAGATGCCTACACCGATTATGTAGCTACGAGATG
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                                                                                                                                                                                                                       GAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAAACATCCAAATCTTGTGAA
                                                                                                                                                                                                                                                                         CCTCATCGAGGTGTTCAGGAGAAAAGGAAAATGCATTTAGTTTTTGAATACTGTGATCA
                                                                                                                                                                                                                                                                                                                         TACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGATGGAGTGATCAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                         375 AGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATCAAGATTTGTGACTT
                                                                                                                                                                                               Gaps
                              2;
                                                                                                                                                                      33.5%; Score 316.8; DB 1; Length 938; 82.9%; Pred. No. 1.1e-69; tive 0; Mismatches 77; Indels 5
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Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
xref="taxon:10090'
          clone="IMAGE:513953"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AV986182.1 GI:19475050
                        /sex="males"
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Ciona intestinalis
                                                                                                                                                                                               Conservative
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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                              Matches
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TITLE
JOURNAL
COMMENT
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LOCUS
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CK472415

AGENCOURT 17613484 NIH MGC_236 Rattus norvegicus cDNA clone
IMAGE:7127611 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACAGAGATATAAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATCAAGATTTGTG 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 Arcercareraaakecaeaaaaaaaararraareaeraaeeaaeererrareaaere 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 AAACCTCTGGACAAGTAGTTAGTGTTAAAAAATTTGTGGAATCTGAAGATGATGATGTTG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGACTCGGGACAAATTGTGGCGCCTCAAAAAATTTGTCGAGTCAGAAGATGACCCGCTGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGAACCTCATCGAGGTGTTCAGGAGAAAAGGAAAATGCATTTAGTTTTGAATACTGTG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGAACCTGATTGAAGTTTTCCGTCGAAAACGCAAATTACATCTTGTGTTCGAGTATTGTG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGATGGAGTGATCA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 ATCATACAGTTTTAAATGAATTGGACAAACACATGAGAGGAGTACCAGAACATGTTA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTICGGGTITGCACAAATICTGA---TICCAGGAGAIGCCIACACCGATTAIGIAGCIA 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACATCCAAATCTTG 190
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cilv41bb8"
/tissue_type="whole animal"
/dev_stage="larva"
/clone_lib="Nori Satoh unpublished cDNA library, larva"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTAGGTGGTACAGAGCACCTGAGCTCCTCGTCGGGGACACTCAGTATGGCCCTCCAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGAGAAGATAGGTAAGATAGGGGAAGGATCTTATGGCATTGTGTTAAATGTCGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 ATGAAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAATGCAGAAACA
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                          Length 598;
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                                                                                                                                                                                                                                                                                                                                                                                          32.5%; Score 306.8; DB 2; Similarity 70.7%; Pred. No. 3.7e-67; 3; Conservative 0; Mismatches 172;
satoh@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1. .598
/organism="Ciona intestinalis"
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Rattus norvegicus
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CK472415.1 GI:40816513
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BP016186
BP016186 Nori Satoh unpublished cDNA library, young adult Ciona intestinalis cDNA clone ciad64e08 5', mRNA sequence.
                                           481 TCTATCTGATAAGGAAAACCCTGGGGGACCTCATTCCCAGGCACCAGCAAGTATTTAGCA 540
                                                                                                                                                                                                                                                      541 TGAATCAGTACTTCAGTGGGGTGAAATTCCAGACCTGAAGACATGGAAACACTTGAGT 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona
1 (bases 1 to 597)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 ATCCTGTTGTTAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACATC 181
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                                                                                                                                                                                    689 GIAACGGGTTTTTCCATGGCATCAGTATACCTGAGGCCAGAAGACATGGAAACTCTTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 ATAACTTGGTGAACCTGATTGAAGTTTTCCGTCGAAAACGCAAATTACATCTTGTGTTTCG
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                                                                                                                                                                                                                                                                                                                                                                                           601 TGAAGTTTCCAAACATCTCCTACTCTGCTCTGGGCTTCTTAAGGG 645
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Pred. No. 1.1e-62;
0; Mismatches 159; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: satch@ascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
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/db_xref="taxon:7719"
/clone="ciad64e08"
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Department of Zoology
Kyoto University
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Best Local Similarity 71.0%;
Matches 397; Conservative
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Ciona intestinalis
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ORGANISM
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TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
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KEYWORDS
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/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="texon:10116"
/clone="lype="kidney, pooled"
/tissue_type="kidney, pooled"
/tissue_type="kidney, pooled"
/lab host="hll OB TonA"
/clone lib="NIH MGC_236"
/note="Organ: Kidney; Vector: pExpress-1; Site_1: EcoRV;
Site_2: Not1; RNA obtained from pooled kidney Fissue from a mix of male and female animals at 8 wk old. Tissues were snap-frozen and kept at -80C for two days before RNA extraction and purification (Tri-reagent method). cDNA was primed using oligo-dr primer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIGURE AND ALGORITHMS AND ALGORITHMS AND CLONED INTO the ECORV/NotI sites of pExpress-1. Size-selection >1.4kb resulted in an average insert size of 2.2 kb. This primary library is normalized (non-normalized primary library is NIH MGC 215) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library."
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                     Contract: Daniels S. Gerhard, Ph.D.
Contract: Daniels S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RmlOA07 Bethesda, WD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:
http://image.lln.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TGGACAGATATCAGAGGGGGTACCAGAGCCTCTCGTGAAGAAGAACATAACTTGGCAGACAC
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Location/Qualifiers
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Best Local Similarity 67.3
Matches 434; Conservative
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Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V.,
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                                                                                                                                 1 Arccaaaacrarcaaccraccarrccrrccacaccccaccrraccaaarccrcaacc
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                                                                                        1 ATGGAAAAGTATGAAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA
                                                                                                                                                                                                                                                                                                             GATAAAATGGTTAAGAAGATCGCTATGCGAGAAATCAAGTTACTAAAGCAACTGCGGCAT
                                                                                                                                                                                                                                                                                                                                                           181 CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAAGGAAAATGCATTTAGTTTTT
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  Length 1956;
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
                                              Indels
Score 275.8; DB 3;
Pred. No. 3.7e-59;
0; Mismatches 282;
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Caenorhabditis elegans
29.2%;
61.6%;
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458; Conser
Query Match
Best Local S:
Matches 458
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GLSGTSLRDCSNVTIDHPRNPGTAIPPLTHULSAVAPGINAAMGTIPGVQNYRVDEKT
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RKEYPKVDVRLPELAYNHLPELRSALEGIARNSRLIKKENKCLSESRIPSLAIDLHAS
SVASHQGAGSPVSDESBADLPRMEHQH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /trānslation="MEKYBNLGLVGEGSYGMVMKCRNKDSGRIVAIKKFLESDDDKMV
KRIAMKBILKLLKQLAHBNLVMLLEVCKKKKRWTLVPERVDHTILDDLKLEPNGLDYQV
VQKYLFQIINGIGFGRHNIIHDIKPENIIVSQSGVVKLCDFGFARTLAAFGEVYD
VVATRWYRAPELLVGDVKYGKAVDIMAIGCLVIEMLMGQPLFPGESDIDQLHHIMTCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNLI PRHQELFYKNPV FAGVRLPEIKDI EAEPLESRY PKLPEVVI SLAKKCLHI DPDK
RPLCADLLHHDFFQMDGFAER YSAGLSSAGCRDQGQRAGPTVTVLFVI TPFAGCQPSA
SYSI CLGSMQSPGQDLASYLADVKLARFSQELQLKI EKDARNNSLPKKFQI RKKEKDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 1956)
Xu,C.S., Chang,C.F., Han,H.P., Wang,G.P., Chai,L.Q., Yuan,J.Y.,
Xu,C.S., Chang,C.F., Ma,H., Wang,L., Wang,S.F., Xing,X.K.,
Shen,G.M., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.
Direct Submission
Submitted (109-SEP-2003) Henan Bioengineering Key Lab, Henan Normal University, No. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTC 15-0CT-2003
                                                                                                               ATTGTATACATGGAGGAAAACCAGAGAACATATTAATCACTAAGCAAGGTGTTATCA 457
                                                                                                                                                                             AGAITTGTGACTTCGGGTTTGCACAAATTCTGA---TTCCAGGAGATGCCTACACCGATT 478
                                                                                                                                                                                                                         517
                                                                                                                                                                                                                                                                   ATGTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGTT 538
                                                                                                                                                                                                                                                                                             518 ATGTGGCCACTAGGTGGTACAGAGCACCTGAGCTCCTCGTCGGGGACACTCAGTATGGCC 577
                                         338 ATCATGTTAAACGTATTGTTTGGCAAGTTCTTCAAGCTGTTCACTTTTGCCATCAGCATA 397
                                                                                     421
GAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACATA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                         Xu,C.S., Chang,C.F., Han,H.P., Wang,G.P., Chai,L.Q., Yuan,J.Y.,
Yang,K.J., Zhao,L.F., Ma,H., Wang,L., Wang,S.F., Xing,X.K.,
Shen,G.M., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.
Liver regeneration after PH
Unpublished
                                                                                     ACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AY383681 1956 bp mRNA line:
Rattus norvegicus LRRGT00026 mRNA, complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="liver regeneration-related"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein_id="AAQ96239.1"
db_xref="GI:37654268"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10116"
1. _1956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=1
product="LRRGT00026"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     || |||| |||| ||| || |||||| CTNCAGTGGATGTGTGGGC 596
                                                                                                                                                                                                                                                                                                                                                           CTTCAGTCGATATATGGGC 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AY383681.1 GI:37654267
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AY383681
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
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REFERENCE AUTHORS

TITLE JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

FEATURES

CDS

ORIGIN

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Marc Vidal Laboratory

Dana Farber Cancer Institute

Ly immy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5739

Email: Marc Vidal@dfci.harvard.edu

Gesigned on the predicted protein encoding ORF. C. elegans ORFeome clouing project: Contact david_hill@dfci.harvard.edu

marc_vidal@dfci.harvard.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="mixed_stage".
/dow_stage="mixed_stage".
/loone_ib="AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into ppc86"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGTTAAAAATTTGTGGAATCTGAAGATGATCCTGTTGTTAAGAAAATAGCACTAAGA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCAATCAAAAAGTTTGTGGAAACTGAAGATGATCCGCATATTAAGAAATTGCGCTACGG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          151 GAAATACGTATGTTGAAGCAATTAAAACATCCAAATCTTGTGAACCTCATCGAGGTGTTC 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAAICAGAAIGCIGAAGCAACIGAAACAICAAAAITIGGITGGATIGAITGAGIGIIC 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 AGGAGAAAAAGGAAAATGCATTTAGTTTTTGAATACTGTGATCATACACTTTTAAATGAG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAACGGAACCGGAAACTTCATCTCGTCTTTTGAACTTTGTGATCGAACTGTACTTCACGAG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 CTGGAAAGAAACCCAAATGGAGTTGCTGATGGAGTGATCAAAAGCGTATTATGGCAAACA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 TIGGAGAAGICCCCAIGGAGIIAACGAIGAACICAIAAAGAAAAIAATITATCAATIG 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTCAAGCTCTTAATTTCTGTCATATACATAACTGTATTCACAGAGATATAAAACCTGAA 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 CTAGAAGCTCTTAAATTCTGTCACAGTCACAAATGTATTCATCAAGAAGTGAAACCGGAA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATATICTAATAACTAAGCAAGGAATAATCAAGATITGTGACTITGGGGTTTGCACAAATT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              451 CTGATTCCAGGAGATGCCTACACCGATTATGTAGCTACGAGATGGTACCGAGCTCCTGAA 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        425 ATAAACACGACGGAAATGTATACTGACTATGTGGCAACTCGTTGGTACCGTAGTCCAGAA 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTICITGIGGGAGATACTCAGTATGTTCTTCAGTCGATATATGGGCTATTGGTTGTGTT 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 365 AACATITICTIGACACGGAATGATCAAGIGAAACTIGGAGATTICGGATTIGCTCGAATA 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAGAAGGGTCTTATGGGGTTGTATTCAAATGCAGAAACAAAACCTCTGGACAAGTAGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l. .565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db xref="taxon:6239"
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tissue_type="whole animal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                         (2003) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="N2"
                                                                                                                                                         Nat. Genet. (2)
Contact: Vidal
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les 379; Conserv
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COMMENT
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485 CTTCTGGTCGGTGATGTTCAATATGGGCCACCTGTAGACATTTGGGCTGTAGGATGTGTA 544
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                              571 TTTGCAGAGCTCCTGACAGGC
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completed: April 22, 2005, 01:23:07 le : 3022.15 secs Search co

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Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 7, Appli
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Sequence 5, Appli
Sequence 30, Appli
Sequence 6, Appli
Sequence 9, Appli
                                                                                                                                          April 21, 2005, 23:37:20 ; Search time 3580.63 Seconds (without alignments) 1602.273 Million cell updates/sec
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                                                                                                                                                                                                                                                                                1 atggaaaagtatgaaaaatt.....aggtacttccgctcaaaagt 945
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-250-889-6
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US-10-766-691-3
US-09-834-496A-3
US-09-834-496A-3
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US-10-766-691-1
US-10-766-691-7
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                                                                                                                                                                                                                                                                                                                                                                                         5633728 seqs, 3035525691 residues
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Listing first 45 summaries
                                                                                                      OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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No.
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Sequence 718, App Sequence 1165, App Sequence 985, App Sequence 40, Appli Sequence 68, App Sequence 68, App Sequence 2447, Ap Sequence 3111, Ap Sequence 3111, Ap Sequence 4192, Ap Sequence 4192, Ap Sequence 4192, Ap

C US-10-295-681-40
C US-10-295-681-40
C US-10-295-681-40
C US-09-954-456-84
US-09-954-456-1165
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US-10-177-293-40
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7 US-10-20-118-668
7 US-10-20-118-668
7 US-10-33-860-3447
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Sequence 24573, A Sequence 5, Appli Sequence 21, Appli Sequence 107, Appli Sequence 112, Appli Sequence 114, Appli Sequence 114, Appli Sequence 28, Appli Sequence 137, Appli Sequence 137, Appli Sequence 137, Appli Sequence 324, Appli Sequence 34, Appli Sequence 31, Appli Sequence 31, Appli Sequence 31, Appli Sequence 40, Appli Sequence 41, Appli Sequence 115, Appli Sequence 1165, Appl

US-10-363-616-146 US-09-960-1079 US-10-134-794-5 US-10-174-794-3 US-10-1369-022-21 US-10-1369-022-21 US-10-757-262-107 US-10-072-036-112 US-10-072-036-114 US-10-072-036-114 US-10-072-036-114 US-10-1072-036-114 US-10-1072-036-114 US-10-1072-036-114 US-10-1072-036-114 US-10-1072-036-114 US-10-1072-036-1137 US-10-641-641-643-1037 US-10-641-643-1037

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RESULT 1

US-10-766-691-11

Sequence 11, Application US/10766691

Sequence 11, Application US/10766691

Publication No. US20080042626A1

GENERAL INFORMATION:

APPLICANT: Turner, C. Alexander Jr.

APPLICANT: Zambrowicz, Brian

APPLICANT: Eachs. Actuar T.

TITLE OF INVENTION: Novel Human Kinase Proteins and

TITLE OF INVENTION: Novel Human Kinase Proteins and

TITLE OF INVENTION: Novel Human Kinase Proteins and

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TITLE OF INVENTION: Novel Human Kinase Proteins and

FILE REPRENCE: LEX-0046-U28

CURRENT APPLICATION NUMBER: US/10/766,691

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 1999-09-28

NUMBER OF SEQ ID NOS: 13

SEQ ID NO 11

LENGTH: 945

TYPE: DAA

ORGANISM: homo sapiens

US-10-766-691-11

Query Match

Matches 945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGGAAAAGTATGAAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA 60

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61 TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT
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APPLICANT: Sands, Arthur T.

TITLE OF INVENTION: Novel Human Kinase Proteins and
TITLE OF INVENTION: Polynucleotides Encoding the Same;
FILE REPERBENCE: LEX-0046-USA;
CURRENT APPLICATION NUMBER: US/10/766,691
CURRENT APPLICATION NUMBER: US/09/671,050
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-28
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASTERQ for Mindows Version 4.0
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100.0%; Pred: No. 4.7e-234;
iive 0; Mismatches 0;
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ORGANISM: homo sapiens
US-10-766-691-5
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Best Local Similarity
Matches 929; Conserv
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                                                       TGCAGAAACAAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAAATTTGTGGAATCTGAAGAT
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Publication No. US20050042626A1
GENERAL INFORMATION:
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nehls, Michael
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
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                            GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACAT
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                                                                                                                         419 CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAAGGAAAATGCATTTAGTTTTT
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APPLICANT: PANZER, Scott R; LINCOLN, Stephen E.;
APPLICANT: ALTUS, Christina M.; DUFOUR, Gerard E.;
APPLICANT: JACKSON, Jennifer L.; JONES, Anissa L.;
APPLICANT: DAM, Tam C.; LIU, Tommy F.;
APPLICANT: BAFFO, Abe; MARMAHA, Rakesh;
APPLICANT: GAFFO, Abe; MARMAHA, Rakesh;
APPLICANT: GERSTIN, Jr. Edward H.; PERALTA, Careyna H.;
APPLICANT: GERSTIN, Jr., Edward H.; PERALTA, Careyna H.;
APPLICANT: DAVID, Marie H.; LEWIS, Samantha A.
TITLE OP INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            901 GAAGGAAGAACAGAAGACGCCAACAG 927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/10250889
Publication No. US20040115629A1
GENERAL INFORMATION:
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                                                   AACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: INTOKCHALLON,
APPLICANT: NINCKTENIN, Farrah A.; GURURAJAN, Rajagopal
APPLICANT: HAPALIA, April J.A.; GURURAJAN, Rajagopal
APPLICANT: HAPALIA, April J.A.; GURURAJAN, Rajagopal
APPLICANT: HAPALIA, April J.A.; GHAMLA, Narinder K.
APPLICANT: GANDHI, Ameena R.; RAMKUMAR, Jayalaxmi
APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.
APPLICANT: THORNTON, Michael B.; LU, Yan
APPLICANT: BURFOND, Neil; LAL, Preeti G.
APPLICANT: BURFOND, Neil; LAL, Preeti G.
APPLICANT: BURFOND, Neil; LAL, Preeti G.
APPLICANT: GRENNEY, Liam; LU, Dyung Aina M.
APPLICANT: GRENNEY, Liam; LU, Dyung Aina M.
APPLICANT: GRENNEY, Liam; LU, Dyung Aina M.
APPLICANT: GRENNEY, Liam; LU, Dyung Aina M.
APPLICANT: GRENNEY, Liam; LU, Dyung Aina M.
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APPLICANT: GRENNEY, Liam; LU, Dyung Aina M.
APPLICANT: GRENNEY, Liam; LU, Dyung Aina M.
APPLICANT: GRENNEY, Liam; LU, Dyung Aina M.
APPLICANT: GRENNEY, Liam; LU, Dyung Aina M.
APPLICANT: GRENNEY, Liam; LU, Dyung Aina M.
APPLICANT: GRENNEY, Liam; LU, Dyung AING, Junming
TITLE OF INVENTION NUMBER: US 60/220,038
PRIOR APPLICATION NUMBER: US 60/222,112
PRIOR APPLICATION NUMBER: US 60/222,831
PRIOR APPLICATION NUMBER: US 60/222,831
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
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PRIOR FILING DATE: 2000-08-04
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PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: PROGFAMM
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OTHER INFORMATION: Incyte ID No: 1698381CB1
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 30, Application US/10333314
Publication No. US20030211093A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 1790
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                                      671 GTTCTTCAGTCGATATATGGGCTATTGGTTGTGTTTTTGCAGGGTCCTGACAGGCCAGC
                                                                                                                      731 CACTGTGGCCTTGAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACACTAGGAA
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Sequence 9, Application US/10766691

Sequence 9, Application US/20050042626A1

SERENALI INFORMATION:

APPLICANT: Turner, C. Alexander Jr.

APPLICANT: Nemble, Michael

APPLICANT: Sambrowicz, Brian

APPLICANT: Sambrowicz, Brian

APPLICANT: Sambrowicz, Brian

APPLICANT: Sambrowicz, Brian

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APPLICANT: Sambrowicz, Brian

CURRENT APPLICATION: NOVERE: US/10/766,691

PRIOR APPLICATION NUMBER: US/09/671,050

PRIOR APPLICATION NUMBER: US 60/156,511

PRIOR FILING DATE: 1999-09-28

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FRASE FRASEO for Mindows Version 4.0
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Pred. No. 2.5e-210;
0; Mismatches 0;
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Best Local Similarity 90.8%;
Matches 945; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            Remaining Prior Application data removed - See File Wrapper or PALM
NUMBER OF SEQ ID NOS: 113
SOFTWARE: PERL Program
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.9%; Score 868.8; DB 18; Length 1678; ilarity 99.2%; Pred. No. 4.5e-218; Conservative 0; Mismatches 2; Indels 5;
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; OTHER INFORMATION: Incyte ID No: LI:058298.1:2001JAN12
US-10-250-889-6
             PRIOR FILING DATE: 2001-09
PRIOR FILING DATE: 2001-09
PRIOR FILING DATE: 2001-01-01
PRIOR FILING DATE: 2001-01-01
PRIOR FILING DATE: 2001-01-01
PRIOR FILING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/261,865
PRIOR FILING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-17
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    APPLICATION NUMBER: PCT/US02/01009
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ORGANISM: Homo sapiens
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Best Local Simi]
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; TITLE OF INVENTION: Polynucleotides Encoding the Same; FILE REFERENCE: LEX-0046-USA; CURRENT APPLICATION NUMBER: US/10/766,691 ; CURRENT FILING DATE: 2004-01-28 ; PRIOR APPLICATION NUMBER: US/09/671,050 ; PRIOR PILING DATE: 2000-09-27 ; PRIOR FILING DATE: 1999-09-28 ; NUMBER OF SEQ ID NOS: 13 ; SCFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 3 ; LENGTH: 1068 ; TYPE: DNA ; ORGANISM: homo sapiens US-10-766-691-3	Query Match 87.1%; Score 823; DB 19; Length 1068; Best Local Similarity 90.6%; Pred. No. 4.2e-206; Matches 929; Conservative 0; Mismatches 0; Indels 96; Gaps .1;	Oy 1 ATGGAAAAGTATGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTCTATTCAAA 60	Qy 61 TGCAGAAACCACTGGACAAGTAGTAGTAGAAAAAAATTTGTGGAATCTGAAGAT 120 	OY 121 GATCCTGTTGTTAAGAAATAGCACTAAGAGAATACGTATGTTGAAGCAATTAAAACAT 180	Oy 181 CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAAGGAAAATGCATTTAGTTTTT 240	Oy 241 GAATACTGATCATACACTTTTAAATGAGCTGGAAAGAACCCAAATGGAGTTGCTGAT 300 241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAA	Oy 301 GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360	OY 361 AACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATC 420	421 AAGATTTGTGACTTTGCACAAATTCTGATTCCAGGAGATGCCTACACCGATTAT 480	Qy 481 GTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGTTCT 540 Db 481 GTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGTTCT 540	Qy 541 TCAGTCGATATATGGGCTATTGGTTGTTTTTGCAGAGCTCCTGACAGGCCACTG 600 bb 541 TCAGTCGATATATGGGCTATTGGTTGTTTTTTGCAGAGGCTCCTGACAGGCCACTG 600	Qy 601 TGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACACT 650
Oy 181 CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAGGAAAATGCATTTAGTTTTT 240 Db 181 CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAGGAAAATGCATTTAGTTTTT 240 OY 241 GAATACTGTGATCATACACTTTTAAATGAGGAAAAGGAAAATGGAGTTTTTT 240 Db 241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGGAAATGGAGTTGCTGAT 300 OY 301 GGAGTGATCAAAAGCGTATTATGGCAAACGCTCTTAATTTCTGTCATATACAT 360 Db 301 GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAATTTCTGTCATATACAT 360 OY 361 AACTGTATTCACAAAGCGTATTAAAAACCTGAAAATATTCTAATTTCTGTCATATACAT 360 Db 361 AACTGTATTCACAAGAGATATAAAAACTGAAAATATTCTAATAAACTAAGGAAGG	OY 421 AAGATTTGIGACTTCGGGTTTGCACAAATTCTGATTCCAGGGGATGCCTACACCGATTAT 480	Oy 481 GTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGTTCT 540	Oy 541 TCAGTCGATATATGGGCTATTGGTTGTTTTTGCAGAGCTCCTGACAGGCCACTG 600	OY 601 TGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACACT 650	Qy 651	Oy 651	OY 685 AAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAAGACATGGAAACTCTT 744	OY 745 GAGGAAAGTTCTCAGATGTTCATCCTGTGGCTCTGAACTTCATGAAGGGTGTCTGAAG 804	OY 805 ATGANTCCAGATGACAGATTAACCTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTCT 864	OY 865 TTTCAAGAGGCCCAATTAAAAGAAAAGCACGTAATGAAGGAAG	Qy 925 CAGGTACTTCCGCTCAAAAGT 945 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 6 US-10-766-691-3 Sequence 3, Application US/10766691 Sequence 3, Application US/10766691 Sequence 3. Application No. US20050042626A1 GENERAL INFORMATION: APPLICANT: Donoho, Gregory APPLICANT: Turner, C. Alexander Jr. APPLICANT: Friedrich, Glenn APPLICANT: Sands, Arthur T. APPLICANT: Sands, Arthur T. APPLICANT: Sands, Arthur T. APPLICANT: Sands, Arthur T.

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                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 1, Application US/09834496A; ; Patent No. US/2020090701A1; ; Patent No. US/2020090701A1; ; APPLICANT: Kapeller-Libermann; TITLE OF INVENTION: 14257 NOVEL PROTEIN KINASE MOLECULES AND TITLE OF INVENTION: THEIR USES THEREFOR; FILE REFERENCE: 38152000900; CURRENT APPLICATION NUMBER: US/09/834,496A; CURRENT APPLICATION NUMBER: 05/01-04-13; PRIOR PILING DATE: 2000-04-13; PRIOR FILING DATE: 2000-04-13; NUMBER OF SEQ ID NOS: 7; SOFTWARE: FastSEQ for Windows Version 4.0; tangent of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control
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68.5%; Score 647; DB 9; I
Best Local Similarity 99.2%; Pred. No. 8.8e-160;
Matches 650; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: (129)...(815)
US-09-834-496A-1
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ORGANISM: Homo sapiens
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GAGGAAAAGTTCTCAGATGTTCATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAG
                                                                                                                                                       ATGAATCCAGATGACAGATTAACCTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTCT
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TITLE OF INVENTION: 14257 NOVEL PROTEIN KINASE MOLECULES AND
TITLE OF INVENTION: 14257 NOVEL PROTEIN KINASE MOLECULES AND
TITLE OF INVENTION: THERE USES THEREFOR
CURRENT APPLICATION NUMBER: US/09/834,496A
CURRENT APPLICATION NUMBER: 00/196,910
PRIOR FILING DATE: 2001-04-13
PRIOR FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 7
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 687
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99.2%; Pred. No. 7.8e-160;
iive 0; Mismatches 5;
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Best Local Similarity 99.2
Matches 650; Conservative
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ORGANISM: Homo sapiens
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481 GTAGCTACGAGATGCTACCTGAGCTTCTTGTGGGAGATACTCGGTATGGTTCT 540 	ò 8	421 AAGATTTGTGACTTCGGGTTTTGGACAAATTCTG
	8 8	454 453 618 TCCTTGATTTGACCTTCTGAATTCTTTTTCTGCCAATTCAGAGATTTTT 677
TGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACACTAGGAA 655	8 8	4
	q	678 CTCCTGGCTTGGATCCATTGCTGACACAGTGTTTCACCATGGGGCCCAGGCTCATCTCGA 737
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sequence 15, Application us/10/000031 Publication No. US20050042626A1	ò	454 453
ENERAL INFORMATION: APPLICANT: Donoho, Gregory	QΩ	798 AGCCACCGTGCCCAGATTTTTCAAACAATAACTACTGAGAGCTCACAAGATTGTTT 857
<pre>lufiler, c. Alexander Nehls, Michael Friedrich, Glenn Zambrowicz, Brian</pre>	ර සි	454
APPLICANT: Sands, Arthur T. TITLE OF INVENTION: Novel Human Kinase Proteins and TITLE OF INVENTION: Polynucleotides Encoding the Same	ි ර	GATTATGTAGGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCGTAT
CURRENT APPLICATION NUMBER: US/10/766,691 CURRENT FILING DATE: 2004-01-28 PRIOR APPLICATION NUMBER: US/09/671,050	ò	GGTTCTTCAGTCGATATATGGCTATTGGTTGTTTTTTGCAGAGCTCCTGACAGGCCAG
FAILOR FILLING DATE: 1999-09-28 NUMBER OF FELL OF THE THE THE THE THE THE THE THE THE THE	8 & 8	CCACTGGGCCTGGAAATCAGATGTGGACTTTATCTGATAATCAGACTT 650
SEQ ID NO 13 LEGISTR: 1819 LEGISTR: 1819	ò	1
; TYPE: UNA SAGANISM: homo sapiens US-10-766-691-13	අු	
13.7%; Score 507; DB 19; Length 1819;	ý d	651
GABARGTATGAAAATTAGCTAAGACTGGAAAGGGTCTTATGGGGTTGTATTCAAA	÷ 8	679 ATCTTTAAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAAGACATGGAA 738
138 ATGGAAAAGTATGAAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTGAA 197 61 TGCAGAAACAAAACCTCTGGACAAGTAGTAGTGGTTAAAAAATTTGTGGAATCTGAAGAT 120 	λ dd	739 ACTCTTGAGGAAAAGTTCTCAGATGTTCATCCTGTGGCTCTGAACTTCATGAAGGGGTGT 798
98 TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 257 21 GATCCTGTTGAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACAT 180	ò	CTGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTCCTGGAGAGCTCCTACTTT 85
	a &	
181 CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAGGAAAATGCATTTAGTTTTT 240 	. ପ୍ର	
241 GAATACTGTGATCATATTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT 300 	රු සි	919 CGCCAACAGGT 929
301 GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360 	RESULT US-10-7 ; Seque	RESULT 10 US-10-766-691-1 ; Sequence 1, Application US/10766691 ; Publication No. US20050042626A1

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the Same
        Polynucleotides Encoding
               FILE REFERENCE: LEX-0046-USA
CURRENT APPLICATION NUMBER: US/10/766,691
FUNRENT FILING DATE: 2004-01-28
PRIOR APPLICATION NUMBER: US/09/671,050
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 7
LENGTH: 594
                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-691-7
       TITLE OF INVENTION:
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US-10-363-616-146
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LENGTH: 1612
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APPLICANT: Donoho, Gregory
APPLICANT: Donoho, Gregory
APPLICANT: Nehls, Michael
APPLICANT: Nehls, Michael
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Novel Human Kinase Proteins and
TITLE OF INVENTION: Novel Human Kinase Proteins and
TITLE OF INVENTION: Novel Human Kinase Proteins and
TITLE OF INVENTION: Novel Human Kinase Proteins and
TITLE OF INVENTION: Novel Human Kinase Proteins and
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TITLE OF INVENTION: Novel Human Kinase Proteins and
TITLE OF INVENTION NOVERE: US/09/671,050
PRIOR PELICATION NUMBER: US/09/671,050
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
SEQ ID NO 1
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Publication No. US20050042626A1
GENERAL INFORMATION:
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, Gregory
APPLICANT: Turner, Gregory
APPLICANT: Turner, Gregory
APPLICANT: Zambrowicz, Glenn
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Novel Human Kinase Proteins and
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Best Local Similarity 99.8
Matches 455, Conservative
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; ORGANISM: homo sapiens
US-10-766-691-1
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US-10-766-691-7
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61 TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
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                                                       Gaps
                                                  0,
             Length 594;
Query Match 48.1%; Score 454.4; DB 19; Length Best Local Similarity 99.8%; Pred. No. 4e-109; Matches 455; Conservative 0; Mismatches 1; Indels
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Publication No. US20040044181A1
Publication No. US20040044181A1
Publication No. US20040044181A1
TERECTION TO USE NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-113 (793)
CURRENT APPLICATION NUMBER: US/10/363,616
PRIOR APPLICATION NUMBER: 03/654,935
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 490
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (463)..(1539)
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LENGTH: 1363
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                                               44.0%; Score 415.4; DB 17; Length 1612; 66.7%; Pred. No. 1.3e-98; ative 0; Mismatches 301; Indels 3;
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                                                                         Best Local Similarity 66.7 Matches 609; Conservative
US-10-363-616-146
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RESULT 13 US-09-960-706-1079

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APPLICANT: Munger, william E.

TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplass;
TITLE OF INVENTION: Gene Expression Profiles
FITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5029-010S
CURRENT APPLICATION NUMBER: US/09/960,706
CURRENT FILING DATE: 2001-09-24
PRIOR PAPLICATION NUMBER: 60/223,323
PRIOR FILING DATE: 2000-08-07
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 43.8%; Score 413.8; DB 10; Length Best Local Similarity 66.6%; Pred. No. 3e-98; Matches 608; Conservative 0; Mismatches 302; Indels
Sequence 1079, Application US/09960706
Publication No. US20030134280A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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949 GACCCTGTCATAAAGAAATTGCCCTTCGGGAAATCCGAATGCTCAAGCAACTCAAGCAT 1008
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                                                                                                                                                                                                                                                        301 GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT
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                                                                                                            .009 CCCAACCTTGTTAACCTCCTGGAAGTCTTCAGGAGGAAACGGAGGCTTCACCTGGTGTTT
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; Sequence 5, Application US/10174794
; Publication No. US20030166220A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REPERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174,794
; CURRENT PILING DATE: 1999-10-01
; PRIOR FILING DATE: 1999-10-01
; PRIOR FILING DATE: 1999-10-02
; RIOR FILING DATE: 1999-10-02
; RIOR FILING DATE: 1999-10-02
; NUMBER: OF SEQ ID NOS: 16
; SOFTWARE: FASISEQ for Windows Version 4.0
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                                                                                   937 CCAGACCCTGAAGATATGGAACCACTTGAATTAAAATTCCCAAACATCTCTTATCCTGCC 996
877 CTCATTCCTAGGCACCAGCAAGTGTTTAGCACGAATCAGTACTTCAGTGGAGTGAAAATT 936
                                              718 CCTGAGCCAGAAGACATGGAAAACTCTTGAGGAAAAGTTCTCAGGATGTTCATCCTGTGGCT 777
                                                                                                                                         CTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAA 837
                                                                                                                                                                                                                                     KITS, AND METHODS FOR
I, PREVENTION, AND THERAPY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TGCAGAAACAAAACTGTGGACAAGTAGTAGCTGTTAAAAATTTGTGGAATCTGAAGAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Endege, wilson
APPLICANT: Endege, wilson
TITLE OF INVENTION: LOBENTIFICATIONS, KITS,
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: NRI-007BGN
CURRENT PAPLICATION NUMBER: 90/785,930
PRIOR PILING DATE: 2003-02-04
PRIOR PELING DATE: 2003-02-04
PRIOR PELING DATE: 2000-03-16
PRIOR PILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
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LOCATION: 1, 2, 3, 2940, 2941, 2942, 2943, 2944

COTHER INFORMATION: n = A,T,C or G

US-10-357-930-24573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24573, Application US/10357930 Publication No. US20040259086A1 GENERAL INFORMATION:
APPLICANT: Schlegel. Robert APPLICANT: Endege, Wilson
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                                                                                             Length 1701;
                                                                                           Query Match 30.4%; Score 287; DB 16; Length 1 Best Local Similarity 59.1%; Pred. No. 8.7e-65; Matches 510; Conservative 0; Mismatches 350; Indels
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; LENGTH: 1701
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; ORGANISM: Orcytolagus cuniculus
US-10-174-794-5
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Sequence 112, Appl
Sequence 114, App
Sequence 115, App
Sequence 131, Appl
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                                                                                                          April 21, 2005, 20:27:40; Search time 178.912 Seconds (without alignments) 8642.674 Million cell updates/sec
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Compugen Ltd.
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Listing first 45 summaries
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APPLICANT: Donoho, Gregory
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Tanha, Michael
APPLICANT: Anabrowicz, Brian
APPLICANT: Sands, Arthur T.
ITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
ITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
ITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
ITLE OF INVENTION: No. 6716616el Human Kinase Proteins
FILE REFERENCE: LEX-0046-USA
CURRENT APPLICATION NUMBER: US/09/671,050
CURRENT APPLICATION NUMBER: US 60/156,511
PRIOR APPLICATION NUMBER: US 60/156,511
PRIOR APPLICATION NUMBER: US 60/156,511
PRIOR APPLICATION NUMBER: US 60/156,511
SEQ ID NO 11
LENGTH: 945
LENGTH: 945
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100.0%; Pred. No. 6.8e-258;
tive 0; Mismatches 0;
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US-09-949-016-181
US-09-949-016-5854
US-08-154-915-1
US-08-154-915-1
US-08-46-361A-37
US-08-46-361A-37
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US-09-861-13423
US-09-81-861-4
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ORGANISM: homo sapiens
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APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nehls, Michael
APPLICANT: Sambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
TITLE OF INVENTION: No. 6017616el Human Kinase Proteins and
TITLE OF INVENTION: No. 6017616el Human Kinase Proteins and
TITLE OF INVENTION: NO. 661066 USC
CURRENT APPLICATION NUMBER: US 60166,511
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEG ID NOS: 13
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GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCT
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Best Local Similarity
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APPLICANT: Duncho, Gregory
APPLICANT: Turther, C. Alexander Jr.
APPLICANT: Turther, C. Alexander Jr.
APPLICANT: Turther, C. Alexander Jr.
APPLICANT: Turther, Glenn
APPLICANT: Exiderich, Glenn
APPLICANT: Sambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0046-USA
CURRENT APPLICATION NUMBER: US/09/671,050
CURRENT PILING DATE: 2001-06-11
PRIOR PRILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FRASESQ for Windows Version 4.0
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90.6%; Pred. No. 2.9e-223;
cive 0; Mismatches 0;
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Best Local Similarity 90.6
Matches 929; Conservative
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ORGANISM: homo sapiens
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APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nehls, Michael
APPLICANT: Fitadrich, Glenn
APPLICANT: Fitadrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
TITLE OF INVENTION: Polynucleotides Encoding the Same
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0046-USA
CURRENT APPLICATION NUMBER: US/09/671,050
CURRENT FILING DATE: 2001-06-11
PRIOR FILING DATE: 1999-09-28
MUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 1041
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90.8%; Pred. No. 8.3e-228;
iive 0; Mismatches 0;
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Best Local Similarity 90.8°
Matches 945; Conservative
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ORGANISM: homo sapiens
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                                                                                                                  0; Indels 402;
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                                                                                      Score 507; DB 4; I
Pred. No. 1.6e-133;
0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                      53.7%;
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Best Local Similarity 69.8
Matches 929; Conservative
                                    TYPE: DNA
ORGANISM: homo sapiens
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LENGTH: 1819
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US-09-671-050-13
US-09-671-050-13
Sequence 13, Application US/09671050
Patent No. 6716616
GENERAL INFORMATION:
APPLICANT: Donoho, GEGOCY
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: APPLICANT: Michael
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
TITLE OF INVENTION: Polymucleotides Encoding the Same
TITLE OF INVENTION: Polymucleotides Encoding the Same
CURRENT APPLICATION NUMBER: US/09/671,050
CURRENT APPLICATION NUMBER: US 60/156,511
PRIOR FILING DATE: 2001-06-11
PRIOR FILING DATE: 1999-09-28
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APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Michael
APPLICANT: Eriedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Polynucleotides Encoding the Same
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REPRENCE: LEX-0046-USA
CURRENT APPLICATION NUMBER: US/09/671,050
CURRENT FILING DATE: 2001-06-11
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
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Best Local Similarity 99.8%; Pred. No. 7.8e-119;
Matches 455; Conservative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 7, Application US/09671050; Patent No. 6716616; GENERAL INFORMATION:
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TYPE: DNA
ORGANISM: homo sapiens
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                                                                               .098 GAGACGGGGTTTCGCCATGTTGACCAGGCTGGTCTCGAACTCTTGACGTCAAGTGATCCA
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Patent No. 6716616
GENERAL INFORMATION:
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; ORGANISM: homo sapiens
US-09-671-050-1
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Patent No. 6428994
GENERAL INFORMATION:
TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
FILE REFERENCE: 13761-707
CURRENT APPLICATION NUMBER: US/09/411,628
CURRENT FILING DATE: 1999-10-01
FARLIER APPLICATION NUMBER: US 60/102,906
FARLIER FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 16
SOUTHWARE: FastSEQ for Windows Version 4.0
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Pred. No. 4e-71;
0; Mismatches 350; Indels
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Best Local Similarity 59.1%;
Matches 510; Conservative (
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LENGTH: 1701
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Patent No. 6812339

GENERAL INFORMATION:
PAPLICART: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR PLILNG DATE: 2000-10-20

PRIOR PLILNG DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 1681

LENGTH: 1177
                                                                                                             361 AACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGGAATAATC 420
                                                              AACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATC 420
GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTTCTGTCATATACAT 360
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Pred. No. 1.3e-107;
0; Mismatches 301;
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Best Local Similarity 66.7%;
Matches 609; Conservative 0
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; ORGANISM: Human
US-09-949-016-1681
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GAATTTGTTGACCACACGATTCTTGATGACTTGGAACTCTTTCCAAATGGACTAGATGAC 300
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                                               GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT
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GENERAL INFORMATION:
TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES;
FILE REFERENCE: 13761-707
CURRENT APPLICATION NUMBER: US/10/174,794
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US/09/411,628
PRIOR APPLICATION NUMBER: US/09/411,628
PRIOR PILING DATE: 1999-10-01
PRIOR PILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
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; ORGANISM: Orcytolagus cuniculus
US-10-174-794-5
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                                                                                                                                                TGCAGAAAAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAGGAAAATGCATTTAGTTTTT
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Sequence 3, Application US/09411628

Sequence 3, Application US/09411628

BERNEAL INFORMATION:
TITLE OF INVERMION: CDNA, GENOMIC, AND PREDICTED PROTEIN
TITLE OF INVERMION: SEQUENCES OF LEARNING-INDUCED KINASES
FILE REFERENCE: 13761-707

CURRENT APPLICATION NUMBER: US/09/411,628

CURRENT FILING DATE: 1999-10-01

EARLIER APPLICATION NUMBER: US 60/102,906

EARLIER FILING DATE: 1999-10-02
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                                                                                                                                                                                          HILE OF INVESTITY OF Southern California
TITLE OF INVESTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
TITLE OF INVESTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
TITLE OF INVESTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
FILE REFERENCE: 13761-707
CURRENT APPLICATION NUMBER: US/10/174,794
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US/09/411,628
PRIOR APPLICATION NUMBER: US 60/102,906
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 3080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3080;
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              1089 CTCCTACACCATGATTTCTTTCA 1111
                                                                                                                            Sequence 3, Application US/10174794
Patent No. 6664086
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Orcytolagus cuniculus
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; LOCATION: (249)...(1949)
US-10-174-794-3
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                                                                                                                                                                                                                                                               Length 3080;
                                                                                                                                                                                                                                                        Score 287; DB 3; Length 30
Pred. No. 5.4e-71;
0; Mismatches 350; Indels
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 3080
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                                                                                        TYPE: DNA ORCYtolagus cuniculus
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 59.1%;
Matches 510; Conservative
                                                                                                                                        ; FEATURE:
; NAME/KSY: CDS
; LOCATION: (249)...(1949)
US-09-411-628-3
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CTATTTCCTGGAGATTCTGATATTGATCAGCTATATCATTATGATGTGTTTTAGGTAAT 1035
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                                                                                             736 AATATCATACACAGAGATATAAAGCCAGAGAATATATTAGTCTCCCAGTCTGGCGTTGTC 795
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                              CTGAACTICATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAA
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; Sequence 9, Application US/08874347
; Patent No. 5863741
; GENERAL INFORMATION:
APPLICANT: Limper, Andrew H.
APPLICANT: Thomas Charles F.
APPLICANT: Thomas Charles F.
APPLICANT: Gustafson, Michael P.
TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS
TITLE OF INVENTION: CARINII
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS: 26
CORRESPONDENCE ADDRESS: 16
CORRESPONDENCE ADDRESS: 16
STREET: 60 South Sixth Street, Suite 3300
CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE CORRESPONDENCE 
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COMPUTER: IBM Compatible
COMPAGE: IBM COMPAGE: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,347
CLASSIFICATION: 435
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REGISTRATION VINDBER: 34,812
REFERENCE/DOCKET NUMBER: 07039/055001
TELECOMMUNICATION INFORMATION:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   612-288-9696
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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TELEFAX: 6
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COUNTRY:
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

RIOR APPLICATION NUMBER: 60/241,755

RIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NGS: 207012.

SOFTWARE: FRASESQ for Windows Version 4.0
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Patent No. 6812339
GENERAL INFORMATION:
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ORGANISM: Human
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61 TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAATTTGTGGAATCTGAAGAT 120
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                                                                                                                                                                                                                                               APPLICANT: Leof, Edward B.
APPLICANT: Thomas, Charles F.
APPLICANT: Gustafson, Michael P.
TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS
TITLE OF INVENTION: CARINII
NUMBER OF SEQUENCES: 26
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0; Mismatches 402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/093,522
FILING DATE: 08-JUN-1998
CLASSIFICATION INTER: 08-JUN-1998
                                                     835 AAAAAAGCTCTCGATCATCCTTATTTTGATGATTT
           832 TCCCAACTCCTGGAGAGCTCCTACTTTGATTCTTT
                                                                                                                                                                                                                                                                                                                                                                                              SSE: Fish & Richardson P.C., P.A.
: 60 South Sixth Street, Suite 3300
Minneapolis
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Pred. No. 1.4
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APPLICATION NUMBER: 08/874,347
FILING DATE: 13-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ellinger, Mark S.
                                                                                                                                                            Sequence 9, Application US/09093522
Patent No. 6015700
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ellinger, Mark S.
REGISTRATION NUMBER: 34,812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-335-5070
                                                                                                                                                                                                                               Andrew H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Coding Sequence
LOCATION: 1...900
OTHER INFORMATION:
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Best Local Similarity 52.3%;
Matches 458; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Fish & Ri
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APPLICANT:
                                                                                                                                            US-09-093-522-9
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Pred. No. 1.4e-38;
0; Mismatches 402;
                                                                                                                                                                       NAME/KEY: Coding Sequence LOCATION: 1...900
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 52.3%;
Matches 458; Conservative (
      9
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 903 base pairs
TYPE: nucleic acid
STRANUBENESS: aingle
TOPOLLGY: linear
                                                                                                                                                                                       ; LOCATION: 1...900
COTHER INFORMATION:
US-08-874-347-9
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181 GATAATGTTAGACTTTTGAATATAATTCATCAAGAGTCACGTTTATATCTTGTTTTT 240

181 CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAGGAAAATGCATTTAGTTTTT

GAATTTCTTGATCTTGATTAAAAGTATATGAATAGTATTCCAAAGGACATGATGCTT 300

241

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295 GCTGATGGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCAT 354

 601 AAGCCATTATTTCCAGGTGATTCTGAAATTGATGAAATATTTAGAATATTTAGAATATTA 660

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592 CAGCCACTGTGGACCTGGAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACACTA

TATGGTTCTTCAGTCGATATATGGGCTATTGGTTGTGTTTTTGCAGAGCTCCTGACAGGC 591

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Search completed: April 22, 2005, 01:29:34 Job time : 183.912 secs

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Adoo1536 Human cyc Adoo1535 Human cyc Ado1535 Human pro Ada29746 Rabbit KK Ada29745 Rabbit KK Ada29155 Human 162 Adg89155 Human 102 Adg89155 Human 102 Adg871263 Prosophil Ada57213 Human NKI Ads6724 Polynucle Ab112602 Drosophil Acn42574 Human dia Ada21207 Rat lost Ada571207 Rat lost Ada670329 DNA encod Ad44672 Novel pro Ad129370 Human MAR

Adol1537 Human cyc Aa237835 Cyclin-de Aav71074 Green flu Aav71073 CDK2-gree Abz83372 Toxicolog Abg60787 Human 10C

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Minimum I Maximum I

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Database

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated human kinase polynucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases.
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                                                                                                                                                                                                                                                                                                                                                           Human; kinase; gene therapy; bioreactor; mental disorder; biological disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .945
/*tag= a
/product= "Human kinase #6"
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ADC77658
ADQ89155
ABL12603
AAZ51208
                                                                             ADI57213
AAS06724
ABL12602
ACN42574
AAZ51207
AAZ51206
AAS70329
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AAX07476
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AAZ37835
AAV71074
AAV71073
ABZ83372
ABZ83372
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P-PSDB; AAE00495.
WO200123579-A1
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Aad03818 Human kin
Abx08936 CDNA enco
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Aad03816 Human kin
Aad03818 Human kin
Ad40928 Human kin
Ad140928 Human kin
Aa164269 Novel pro
Aa162367 Human MAR
Abx34679 Human mAR
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Aad03818 Human kin
Abz77165 Human kin
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Abz77165 Human kin
Abd93818 Human kin
                                                           April 21, 2005, 20:23:24; Search time 517.228 Seconds (without alignments) 10815.645 Million cell updates/sec
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                                                                                                                 1 atggaaaagtatgaaaaatt......aggtacttccgctcaaaagt 945
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                                                                                                                                                                             8780412
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                            4390206 segs, 2959870667 residues
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Listing first 45 summaries
                                           OM nucleic - nucleic search, using sw model
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AAD3657

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1083
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Score

Result No.

868.8 863

839 823 808 704.4 645.4 643.4 643 559.2 559.2 543.2 507

454.4 454.4 415.4

The present sequence is a cDNA encoding novel human protein (NHP) known as human kinase. The human kinases share structural similarity with cas human kinases. The human kinases of animal kinases.

C animal kinases, more particularly serine or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP concleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the identification of other cellular gene products related to human kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or screening compounds that are useful for treating mental, biological or medical disorders. NHP oligonucleotides are used as probes. The labelled NHP polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP products are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene Sequence 945 BP; 323 A; 165 C; 202 G; 255 T; 0 U; 0 Other; X888888888888888888888888888888

ö 300 120 121 GATCCTGTTGATAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACAT 180 240 240 300 GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACAT 180 360 301 GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATAACAT 360 900 99 099 480 540 540 900 9 AAGATITIGIGACITICGGGITITGCACAAATICTGATICCAGGAGAIGCCTACACGATTAI 480 1 ATGGAAAAGTATGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGGTTGTATTCAAA TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT CCAAATCTTGTGAACCTCATCGAGGTGTTTCAGGAGAAAAAGGAAAATGCATTTAGTTTTT GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAAGGAAAATGCATTTAGTTTTT 601 TGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACACTAGGAAAATTA Gaps AAGATTTGTGACTTCGGGTTTGCACAATTCTGATTCCAGGAGATGCCTACACCGATTAT GTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGTTCT 181 GTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGTTCT .; 0 100.0%; Score 945; DB 4; Length 945; 100.0%; Pred. No. 3.3e-244; ive 0; Mismatches 0; Indels (Best Local Similarity 100. Matches 945; Conservative Query Match 61 121 181 181 241 241 301 421 481 361 421 g ò g

The present sequence is a cDNA encoding novel human protein (NHP) known as human kinase. The human kinases share structural similarity with animal kinases. The human kinases share or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for the diagnosis of fisease, and also as a therapeutic in is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the identification of other cellular gene

661 ATCCCAAGACATCAATCAATCTTTAAAAGTAACGGGTTTTTCCATGGCATCAGTATACCT 720

Disclosure; Page 29-30; 38pp; English.

840 CTGGAGAGCTCCTACTTTGATCTTTTCAAGAGGCCCAAATTAAAAGAAAAGCACGTAAT 900 Location/Qualifiers
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                                                                                                                                     products related to human kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical disorders. NHP oligonucleotides are used as probes. The labelled NHP probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP products are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene
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                                                                                                                                                                                                                                                                                                                                  CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAGGAAAATGCATTTAGTTTTT
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                                                                                                                                                        4; Length 972;
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                                                                                                                                                                            0; Indels
                                                                                                                                                        Score 929; DB 4; Le
Pred. No. 6.8e-240;
                                                                                                              therapy for the modulation of NHP expression
                                                                                                                                              98.3%; Sco. No. 0. 100.0%; Pred. No. 0. 1 Mismatches
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les 929; Conserv
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Human; kinase polypeptide; PKIN-10; gene therapy; Addison's disease; leukaemia; immune disorder; lymphoma; melanoma; developmental disorder; acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension; asthma; Crohn's disease; rheumatoid arthritis; bursitis; atherosclerosis; repaids; psoriasis; Cushing's syndrome; cytostatic; cancer; cirthosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer; cholestasis; cardiant; cardiovascular disorder; Niemann-Pick's disease; lipid disorder; fatty liver; daucher's disease; mycoardial infarction; drug screening; transgenic animal; antiinflammatory; hepatotropic;
                                    CTGGAGAGCTCCTACTTTGATTCTTTTCAAGAGGCCCAAATTAAAAGAAAAGCACGTAAT 900
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CTGGAGAGCTCCTACTTTGATTCTTTTCAAGAGGCCCAAATTAAAAGAAAAGCACGTAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
239. .1267
/*tag= a
/product= "Human PKIN-10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human kinase polypeptide (PKIN-10) cDNA.
                                                                                                                                                                                                GAAGGAAGAACAGAAGACGCCAACAGGT
                                                                                                                                                GAAGGAAGAACAGAAGACGCCAACAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                        standard; cDNA; 1790
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28-JUL-2000; 2000US-0222112P.
04-AUG-2000; 2000US-022831P.
11-AUG-2000; 2000US-0224729P.
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us-10-766-691-11.rng

cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial infarction), and a lipid disorder (e.g., fatty liver, cholestasis, Gaucher's disease, Niemann-Pick's disease). FKIN is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. FKIN is useful for creating knockin humanised animals or transgenic contains to model human diseases, in somatic or general or creating chockin humanised animals or transgenic generate a transcript image of a tissue or cell type, for detecting contains to model human diseases, in somatic or generate a transcript image of a tissue or cell type, for detecting cetc., among normal, carrier or affected individuals, and as hybridisation probes for mapping naturally occurring genomic sequences. PKIN is useful cetchnologies, in PCR technologies, in dipstick, pin, multiformat enzyme linked immunosorbent (ELISA)-like assays and in microarrays utilisaing these tresent sequence is human PKIN-10 cDNA

Sequence 1790 BP; 581 A; 328 C; 366 G; 515 T; 0 U; 0 Other;

; 98.1%; Score 927; DB 6; Length 1790; 100.0%; Pred. No. 3e-239; ive 0; Mismatches 0; Indels 0; Indels Query Match Best Local Similarity 100.0 Matches 927; Conservative

Gaps ò

61 IGCAGAAACAAAACCICTGGACAAGTAGTAGCTGTTAAAAATTTGTGGAATCTGAAGAT 120 ATGGAAAAGTATGAAAAATTAGCTAAAGACTGGAGAAGGGTCTTATGGGGGTTGTATTCAAA

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418 240 181

CCAAATCTTGTGAACTCCATCCAGGTGTTCAGGAAAAAAGGAAATGCATTTAGTTTTT

241

GGAGTGATCAAAAGCGTATTATGGCAAACACTTTCAAGCTCTTAATTTCTGTCATATACAT 360 301

598 420 658 480 718 540

AACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATC 361 599

AAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGATGCCTACACGGATTAT 421

GTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGTTCT GTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGTTCT 481 719

TCAGTCGATATAGGGCTATTGGTTGTTTTTGCAGAGGTCCTGACAGGCCAGTG TGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAAACACTAGGAAAATTA 541 779 601

ATCCCAAGACATCAATCTTTAAAAGTAACGGGTTTTTTCCATGGCATCAGTATACCT ATCCCAAGACATCAATCTTTAAAAGTAACGGGTTTTTCCATGGCATCAGTATACCT 839 199 899

GAGCCAGAAGACATGGAAAACTCTTGAGGAAAAGTTCTCAGATGTTCATCCTGTGGCTCTG GAGCCAGAAGACATGTGAGGAAAGTTCTCAGATGTTCATCCTGTGGCTCTG

721

ABX08936 standard; cDNA; 1678 BP

RESULT 4

ABX08936;

(first entry) 21-JAN-2003

cDNA encoding human DITHP protein #6.

Human; ss; gene; diagnostic and therapeutic; DITHP; cancer; arteriosclerosis atherosclerosis, psoriasis; primary thrombocytopenia; autoimmune; inflammatory; anaemia; asthma; autoimmune thyroiditis; Crohn's disease; diabetes mellitus; glomerulonephritis; gout; stroke; multiple sclerosis; rheumatoid arthritis; uveitis; AIDS; allergy; acquired immunodeficiency disease; neurological disorder; epilepsy; Alzheimer's disease; dementia; mental retardation; gastrointestinal; Parkinson's disease; ulcer; cirrhosis; reproductive; infertility; endometriosis; endocrine disorder; hyperparathyroidism; hyperlipidemia; hypercholesterolaemia; hypoglycaemia; obesity; Reiter's syndrome; connective tissue disorder; osteoporosis; infection.

Homo sapiens.

WO200279473-A2.

10-0CT-2002

09-JAN-2002; 2002WO-US001009

; 2001US-0261622P. ; 2001US-0261864P. ; 2001US-0261865P. ; 2001US-0262164P. ; 2001US-0262164P. 2001US-0262208P 2001US-0262599P 2001US-0262215P 2001US-0263102P 17-JAN-2001; 17-JAN-2001; 17-JAN-2001; 18-JAN-2001; 19-JAN-2001; 19-JAN-2001; 17-JAN-2001; 17-JAN-2001;

2001US-0263063P. 2001US-0263064P. 2001US-0262760P 2001US-0263065P 19-JAN-2001; 2 19-JAN-2001; 2 19-JAN-2001; 2 19-JAN-2001; 19-JAN-2001; 19-JAN-2001; 19-JAN-2001

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(INCY-) INCYTE GENOMICS INC.

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720 958

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19-JAN-2001; 2001US-0263330P

Jones AL; Chen AJ; Dufour GE, Hillman JL, V, Daffo A, Marwaha R, David MH, Lewis SA; Altus CM, I S B, Flores V Peralta CH, Lincoln SE, u TF, Harris Liu TF, Harrie Gerstin EH, Dam TC, Li Chang SC, SR. Panzer

WPI; 2003-040680/03 P-PSDB; ABU05290.

TACCTGAGCCAGAAGATGGAAACTCTTGAGGAAAAGTTCTCCAGATGTTCATCCTGTGG

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TACCTGAGCCAGAAGACATGGAAACTCTTGAGGAAAAGTTCTCAGATGTTCATCCTGTGG

911 CTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCC AACTCCTGGAGGGCTCCTACTTTGATTTCAAGAGGCCCCAAATTAAAAGAAAAGCAC

776 CTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCC

775 910

655 790

GITCITCAGICGAIAIAIGGGCIAIIGGIIGIGIIIIIGCAGAGCICCIGACAGGCCAGC 671 GTTCTTCAGTCGATATATGGGCTATTGGTTGTGTTTTTGCAGAGCTCCTGACAGGCCAGC CACTGTGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACACTAGGAA 731 CACTGTGGCCTTGAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACACTAGGAA

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This invention relates to the cDNA and protein sequences of fifty six polymucleotides for diagnostics and therapeutics (DITHP). The human DITHP polymucleotides and polypeptides are useful for diagnosing, preventing or treating diseases associated with, as well as effects of exogenous compounds, on the expression of human molecules, such as cell compounds, primary thrombocytopenia), autoimmune-inflammatory diseases (e.g. anaemia, asthma, autoimmune thyroiditis, Crohn's disease, diabetes callitus, glomerulonephritis, gout, multiple scalerosis, rheumatory diseases callitus, glomerulonephritis, gout, multiple scalerosis, rheumatorid arthritis, uveitis, acquired immunodeficiency disease; AIDS; allergies; neurological disorders (e.g. stroke, Alzheimer's disease; Alms; allergies; carthritis, treatedation, parkinson's disease, epilepsy), gastrointestinal (e.g. ulcer, cirrhosis), reproductive (e.g. infertility, endometriosis), reproductive (e.g. infertility, endometriosis), reproductive (e.g. infertility, endometriosis), reproductive (e.g. infertility, endometriosis), reproductive (e.g. infertility, endometriosis), connective tissue disorders (e.g. osteoporosis, Reiter's syndrome), or infections (e.g. bacterial), viral, fungal, parasitic, protozoal). The DITHP sequences may be used to converted hybridisation probes useful in chromosomal mapping or naturally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              occurring genomic sequences. They are also useful in designing probes useful in diagnostic assays. The polynucleotides are useful as molecular weight markers, or as antigen to elicit an immune response. The present
New human diagnostic and therapeutic (DITHP) polynucleotides and polypeptides, useful for diagnosing, preventing or treating diseases, e.g. cancer, AIDS, Parkinson's disease, or autoimmune/inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence represents a human diagnostics and therapeutics (DITHP) cDNA
                                                                                                                                                                   Claim 1; Page 267; 331pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence of the invention
                                                                                                     diseases
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AACTCCTGGAGAGCTCCTACTTTGATTCTTTCAAGAGGGCCCAAATTAAAAAGGAAC

836

971

968

GTAATGAAGGAAGAACAGAAGACGCCAACAG 927

835

Gaps 5; Score 868.8; DB 10; Length 1678; Pred. No. 1.4e-223; 0; Mismatches 2; Indels 5; Sequence 1678 BP; 541 A; 308 C; 336 G; 493 T; 0 U; 0 Other; 91.9%; Query Match 91.9 Best Local Similarity 99.2 Matches 925; Conservative

430 418 ATGGAGAAGTATGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA 190 ATCCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAAGGAAAATGCATTTAGTTT 370 431 ATGGAGTGATCAAAAGGGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATAC 490 TGCAGA-AACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGA 119 TGATCCTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTA-TGTTGAAGCAATTAAAAC 178 179 ATCCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAAGGAAAATGCATTTAGTTT 238 ATGGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATAC 358 9 ATAACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAA 1 ATGGAAAAGTATGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA 120 61 311 239 371 299 359 셤 a 셤 ठे 셤 ઠે 셤 ઠે g ð ሯ δ ò

novel Nucleic acids encoding human kinase polypeptides, useful for preventing diagnosing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections. AASO6701-AASO6757 encode for novel human protein kinases #1-57. The protein kinases have been identified as members of the tyrosine or serine/threonine kinase (PTK and STK) families. The polynucleotides encoding protein kinases and the polypeptides may be used in the prevention, diagnosis and treatment of diseases associated with 3xample 1; Fig 1; 433pp; English. P-PSDB; AAU03525.

ATGTAGCTAGCGAGATGGTACCGAGCTCCCTGAACTTCTTGTGGGGAGATACTCCAGTATG 670

610 535

491 ATAACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAA 550

TCAAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGATGCCTACACCGATT 478

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TCAAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGATGCCTACACGATT ATGTAGCTA-CGAGATGGTACCGAGCT-CCTGAACTTCTTGTGGGGAGATACT-CAGTATG

Human; protein kinase; PTK; STK; cancer; cardiovascular disease; metabolic disorder; immune related disease; neurological disorder; neurodegenerative disorder; inflammatory disorder; infectious disease; reproductive disorder; gene therapy; ss. G, Sudarsanam S, Martinez Polynucleotide sequence encoding human protein kinase #25. Manning AAS06725 standard; cDNA; 1083 22-NOV-2000; 2000WO-US032085. 99US-0167482P. (first entry) Whyte D, Clary D; WPI; 2001-343950/36. (SUGE-) SUGEN INC WO200138503-A2. 12-SEP-2001 24-NOV-1999; Plowman GD, Flanagan P, 31-MAY-2001. RESULT 5 원

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61 TGCAGAAACAAAACCTCTGGACAAGTAGTTAGTTAAAAAATTTGTGGAATCTGAAGAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inappropriate kinase expression. For example, they may be used to treat cancers (especially cancers of haematopoietic origin), cardiovascular disease (e.g. atheroscalerosis), metabolic disorders (e.g. diabetes), immune related diseases (e.g. theumatoid arthritis), neurological barkinson's disease), inflammatory disorders (e.g. asthma), inflammatory disorders (e.g. asthma), infectious disease (e.g. HIV) and reproductive disorders (e.g. infertility).

Additionally, polynucleotides encoding protein kinases may be used for polypeptides may be used as antigens in diagnostic assays. The protein kinase against the protein kinase and in assays to identify modulators of protein kinase expression and activity
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                                                                                                                                                                                         Sequence 1083 BP; 366 A; 199 C; 225 G; 293 T; 0 U; 0 Other;
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Best Local Similarity 94.5%;
Matches 927; Conservative C
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906 781 GAAGACATGGAAACTCTTGAGGAAAGTTCTCAGATGTTCATCCTGTGGCTCTGAACTTC 840 ATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTCCTGGAG 846 The present sequence is a cDNA encoding novel human protein (NHP) known as human kinases. The human kinases share structural similarity with than animal kinases. The human kinases or threonine protein kinases. The diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of MHP in the body. The NHP in diagnostic assays, for the identification of other cellular gene products related to human kinases, and as reagents in diagnostic assays, for the identification of other cellular gene products related to human kinases, and as reagents in assays for medical disorders. MHP oligonucleotides are useful for treating mental, biological or medical disorders. MHP oligonucleotides are used as probes. The labelled PNPMP probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations 847 AGCTCCTACTTTGATTCTTTTCAAGAGGCCCAAATTAAAAGAAAAGGACGTAATGAAGGA 901 AGCTCCTACTITIGATTCTTTTCAAGAGGCCCAAATTAAAAGAAAGGAGGTAGTAGAAGGA /product= "Human kinase #5" /note= "The coding region does not include stop codon" New isolated human kinase polynuclectide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases. 'n, Human; kinase; gene therapy; bioreactor; mental disorder; biological disorder; ss. Zambrowicz Friedrich G, Location/Qualifiers AGAAACAGAAGACGCCAACAG 927 981 Claim 1; Page 31-32; 38pp; English. AAD03816 standard; cDNA; 1041 BP Turner CA, Nehls M, 961 AGAAACAGAAGACGCCAACAG 27-SEP-2000; 2000WO-US026621. 99US-0156511P. (LEXI-) LEXICON GENETICS INC. (first entry) ø 1. .1041 /*tag= a 'partial Human kinase cDNA #5. WPI; 2001-266166/27. P-PSDB; AAE00494. WO200123579-A1 Homo sapiens. 28-SEP-1999; 19-JUN-2001 05-APR-2001. 907 787 Donoho G, Sands AT; AAD03816; RESULT 6 요 ò g Š à 셤

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within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP products are used to genetically enginer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression
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                                                                                                                                   Length 1041;
                                                                                                    Sequence 1041 BP; 344 A; 190 C; 228 G; 279 T; 0 U; 0 Other;
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Pred. No. 1.3e-215;
0; Mismatches 0;
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Best Local Similarity 90.8
Matches 945; Conservative
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the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the identification of other cellular gene products related to human kinases, and as reagents in assays for medical disorders. NHP oligonucleotides are used as probes. The labelled NHP probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a cDNA encoding novel human protein (NHP) known as human kinase. The human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "Human kinase #2"
/note= "The coding region does not include stop codon"
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                  901 ATGAATCCAGATGACAGATTAACCTGTTCCCAACTCCTGGAGAGACTCCTACTTTGATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human kinase polynucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases.
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  in vivo that functions supply of NHP to the NHPs are used in gene
                                                                                                                    1 ATGGAAAAGTATGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGGTTGTATTCAAA
                                                                                                                                               TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTTGTGGAATCTGAAGAT
                                                                                                                                                                                      GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACAT
                                                                                                                                                                                                   CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAGGAAAATGCATTTAGTTTTT
                                                                                                                                                                                                                                            CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAAAGGAAAATGCATTTAGTTTTT
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                                                                                          96;
                                                                    Score 823; DB 4; Length 1068;
Pred. No. 2.6e-211;
0; Mismatches 0; Indels 99
                                                    0 U; 0 Other;
                                                                                         0; Indels
products are used to genetically engineer cells bioreactors in the body delivering a continuous body. Nucleotide constructs encoding functional therapy for the modulation of NHP expression
                                              Sequence 1068 BP; 344 A; 197 C; 240 G; 287 T;
                                                                 Query Match
Best Local Similarity 90.6%;
Matches 929; Conservative
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901 ATGAATCCAGATGACAGATTAACCTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTCT 960
                                    human; kinase; phosphatase; KPP; cardiovascular; antiarteriosclerotic; hypotensive; vasotropic; antianflammatory; antianginal; anti-HIV; antialegic; antiasthmatic; immunosuppressive; antithyroid; dermatological; antidabetic; nephrotropic; antigut; gastrointestinal; neuroprotective; osteopathic; antiarthritic; uropathic; ophthalmological; antisheumatic; antiparkinsonian; nootropic; anticonvulsant; hepatotropic; antisheumatic; antibacterial; virucide; protozoacide; fungicide; antibacterial; virucide; protozoacide; fungicide; cardiovascular disease; immune system; neurological; growth; development; cell proliferation; viral; bacterial; fungal; parasitic; protozoan; helminthic infection; transgenic; gene therapy; ss; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel isolated polypeptide which is a human kinase and phosphatase (KPP). The polypeptide of the invention demonstrates cardiovascular, antiarteriosclerotic, hypotensive, vasotropic, antianflammatory, antianginal, anti-HIV, antiallergic, antidasthmatic, immunosuppressive, antithyroid, dermatological, antidabetic, nephrotropic, antigout, gastrointestinal, neuroprotective, osteopathic, antiarthritic, uropathic, ophthalmological, antirheumatic, antiparkinsonian, nootropic, anticonvulsant, hepatotropic, antipsoriatic, haemostatic, cytostatic, antilipaemic, antiparasitic, antihelmintic,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human kinases and phosphatases, useful for diagnosing, treating or preventing atherosclerosis, hypertension, AIDS, allergy, multiple sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Richardson TW, Marquis JP, Swarnakar A, Tang YT;
Emerling BM, Jin P, Wilson AD, Yue H, Gietzen KJ;
Yang YG, Lee SY, Khare R, Elliott VS, Hafalia AJA;
, Ramkumar J, Gururajan R, Tribouley CM, Chien D,
                                                                                                                                                                                                                                                                                                                                             Human kinase and phosphatase KPP-45 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; SEQ ID NO 104; 347pp; English.
                                                                                                                                                                                                                                        standard; cDNA; 1266 BP.
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25-SEP-2002; 2002US-0413910P.
27-SEP-2002; 2002US-0414296P.
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P-PSDB; ADK71868
                                                                                                                                            CAGGT
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Murage J;
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Chang H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibacterial, virucide, protozoacide and fungicide activities. The kinase and phosphatase (KPP) polynuclectides, polypeptides, agonists and antagonists may be useful for diagnosing, treating or preventing disorders such as cardiovascular diseases, immune system disorders, neurological disorders affecting growth and development, cell proliferative disorders and viral, bacterial, fungal, parasitic, protozoan or helminthic infections. Furthermore, the molecules of the invention may be useful for creating transgenic animals to model human disease and during gene therapy. The current sequence is that of a human or human and parameters.
                                                                                                                                                                                                                                                           54 ATGGAAAAGTATGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA 113
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                                                                                                                                                                               Length 1266;
                                                                                                                                                 Sequence 1266 BP; 414 A; 234 C; 254 G; 364 T; 0 U; 0 Other;
                                                                                                                                                                          Score 808; DB 12;
Pred. No. 3.1e-207;
0; Mismatches 0;
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                                                                                                                                                                             85.5%;
                                                                                                                         KPP cDNA of the invention.
                                                                                                                                                                                         Best Local Similarity 89.5
Matches 927; Conservative
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                                                                              GGGGTGTCTGAAGATGAATCAGATGACAGATTAACCTGTTCCCAACTCCTGGAGGCTC
                CATGGAAACTCTTGAGGAAAAGTTCTCAGATGTTCATCCTGTGGCTCTGAACTTCATGAA
                                                                                                                            GGGGTGTCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTCCTGGAGAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Emerling BM, Kable AE, Richardson TW, Becha SD;
Tang YT, Lal PG, Lee SY, Griffin JA, Khare R;
Jin P, Hawkins PR, Swarnakar A, Chawla NK, Tran UK;
, Ding L, Marquis JP, Thornton MB, Forsythe IJ, Lee I
Ramkumar J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human kinases and phosphatases, useful for diagnosing, treating
                                                                                                                                                                                                                                                                                                                                                                                                   Human kinase and phosphatase KPP-41 encoding cDNA SEQ ID NO:94
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/product= "kinase and phosphatase KPP-41"
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                                                                                                                                                                                                            CAGAAGACGCCAACAG 1089
                                                                                                                                                                                                                                                                                                      ADI40928 standard; cDNA; 1429
                                                                                                                                                                                        CAGAAGACGCCAACAG 927
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02-AUG-2002; 2002US-040059P.
02-AUG-2002; 2002US-0400783P.
15-AUG-2002; 2002US-040078P.
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Elliott VS,
Gururajan R,
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Query Match 셤 à d ò g ò 셤

The present sequence encodes a human kinase and phosphatase (KPP)

protein. KPP sequences have cardiovascular, antiarteriosclerctic,

thycotensive, wasotropic, antiinflammatory, antianginal, anti-HIV,

cantiallergic, antiasthmatic, immunosuppressive, antithyroid,

dermatological, antidiabetic, immunosuppressive, antithyroid,

cantificumatic, antidiabetic, immunosuppressive, antithyroid,

cantificumatic, antidiabetic, immunosuppressive, antithyroid,

cantificumatic, antiparkinsonian, nootrobic, anticonvulsant, heperotropic,

cantificumatic, antiparkinsonian, nootrobic, antilipaemic, antiparasitic,

cantificumatic, antibacterial, virucide, protozoacide and fungicide

phosphatase modulators. KPP proteins, polymucleotides, agonists and

associated with aberrant expression of KPP, such as stations and

associated with aberrant expression of KPP, such as cardiovascular

cantagonists can be used for diagnosing, treating or preventing disorders

diseases (e.g. atherosclerosis, hypertension, vasculitis, angina pectoris

consective heart failure), immune system disorders (e.g. AlDS,

allergies, asthma, autoimmune thyroiditis, contact dermatitis, contact

consective heart failure), immune system disorders (e.g. AlDS,

disease, disbaces mellitus, glomerulonephritis, Goodpasture's syndrome,

cout, irritable bowel syndrome, or uveitis, glomerulonephritis,

disease, parkinson's disease, Hultington's disease, dementia or

costeoporosis, pancreatitis, neurological disorders (e.g. Alzheimer's

cycleptroblesterolamia, hyperilipidaemia or cancer), or viral, bacterial,

compounds on the expression of midiale acids and kinases and

compounds on the expression of midiale acids and kinases and

compounds on the expression of midiale acids and kinases and

compounds on the expression of midiale acids and kinases and

compounds on the expression of polymucleotides are also useful in assessing the effects of exogenous

compounds on the expression of midiale acids and kinases and

compounds on the expression of polymucleotides encoding KP 5; SEQ ID NO 94; 330pp; English Claim

Sequence 1429 BP; 466 A; 286 C; 294 G; 383 T; 0 U; 0 Other;

120 300 180 240 309 9 369 360 429 420 489 1 ATGGAAAAGTATGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAAGAT 181 CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAGGAAAATGCATTTAGTTTTT 361 AACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATC 421 AAGAITIGIGACTICGGGITIGCACAAATICIG-----ccaaatcttgtgaacctcatcgaggtgttcaggagaaaaggaaaatgcatttagttttt GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT Gaps Score 704.4; DB 12; Length 1429; Pred. No. 2.7e-179; 0; Mismatches 1; Indels 199; 1; Indels 199; 74.5%; Jest Local Simitaricy of Matches 924; Conservative Similarity 61 121 241 301

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550 GCTCATCTCGAACTTCTGGCCTCAAGTGATCCTTCCACCTCGGCCTCCCAAAGTGCTGGA 609 610 TTACAAGTGTGAGCCACCGTGCCCAGCCAGATTTTTCAAACAATAACTACTGAGAGCTCA 669 463 789 847 643 823 907 703 967 763 883 670 CAAGATIGITITIAGIGGGAACACAATITICGAACAAATICITIGAGAACGCATICCAGGAG 464 AIGCCTACACCGATTATGTAGCTACGAGATGGTACCGAGGTCCTGAACTTCTTGTGGGAG ATACTCAGTATGGTTCTTCAGTCGATATATGGGCTATTGGTTGTGTTTTTGCAGAGCTCC TGACAGGCCAGCCACTGTGGAAAAATCAGATGTGGACCAACTTTATCTGATAATCA GAACACTAGGAAAATTAATCCCAAGACATCAATCTATTAAAAGTAACGGGTTTTTCC ATGGCATCAGTATACCTGAGCCAGAAGACATGGAAACTCTTGAGGAAAAGTTCTCAGATG 764 ITCAICCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGAT 824 TAACCTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTCTTTTCAAGAGGCCCAAATTA AAAGAAAAGCACGTAATGAAGGAAGAAGAAGAGACGCCAACAG 927 454 730 524 584 848 644 704 884 ò g ò q ð g ò 임 ò g δ g à g ð 셤 ઠે a

RESULT 10 AA164248

AAI64248 standard; cDNA; 882 AAI64248;

BP

08-MAR-2002 (first entry)

Human kinase 14257 cDNA.

antidiabetic; neuroprotective; antiarthritic; dermatological; munosuppressive; antinflammatory; antithyroid; antipsoriatic; ophthalmological; antiallergic; antiasthersoclerctic; hypotensive; vasorropic; antiarthythmic; virucide; anorectic; metabolic; munomodulator; analgesic; cellular proliferative disorder; cancer; acute lymphoblastic leukaemia; Hodgkin's disease; bone metabolism disorder; osecoprosis; immune system disorder; inflammatory; diabetes mellitus; osteoarthritis; asthma; inflammatory; diabetes mellitus; osteoarthritis; asthma; cardiovascular disorder; hypertension; coronary artery disease; endothelial cell disorder; psoriasis; ss. Protein kinase; enzyme; cytostatic; osteopathic; hepatotropic;

Homo sapiens

Location/Qualifiers /*tag=

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488
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                       Human, mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acida encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease,
                                                                                                                                                                                                                                                                                              AAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGATGCCTACACCGATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence encodes a novel protein kinase. The nucleic acids and the protein kinases they encode may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and
                                                                                                          GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT
                                                                                                                                                         AACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAAATC
                                                                                                                                                                                                         AACTGTATTCACAGAGATGTAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATC
                                                                                                                                                                                                                                                 AAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGATGCCTACACCGATTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACACTAGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated 14257 polypeptide and nucleic acid encoding it. The 14257 protein is a protein kinase that acts as a modulating agent in regularing a variety of callular processes, including cell proliferation, differentiation, growth and division. The activity of the protein of the invention may be described as; cytostatic; osteopathic; hepatotropic, antidiabetic, neuroprotective, antiarthritic; antiparthritic; antiparthritic; antiparthritic; antiparthritic; antiparthritic; antiparthritic; antiparthritic; antiparthritic; antiparthritic; antiparthritic; antiparthritic; antiparthritic; antiparthritic; antiparthritic; antiparthritic; antiparthritic; antiparthritic; antiparthritic; antiparthritic; antiparthritic; antiparthritic; immunoaughensive; ansotropic; antiarthritic; virucide; antiparthritic; metabolic; immunomodulator and analgesic. The protein of the invention may act as a novel diagnostic target or therapeutic agent invention may act as a novel diagnostic target or therapeutic agent controlling certain disorders, for example kinase-associated or other lasorders such as cancers e.g. acute lymphoblastic leukemia or Hodgkin's disease. Other disorders include bone metabolism disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   osteoporosis, disorders of the immune system, e.g. inflammatory, diabetes mellitus, osteoarthritis and asthma. Proteins of the invention any also be of use as therapeutic agents in cardiovascular disorders such as hypertension and coronary artery disease, and some endothelial cell disorders, including psoriasis. The current sequence represents a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New 14257 polypeptides (protein kinases), useful as diagnostic targets and therapeutic agents for controlling cellular proliferative and/or differentiative disorder, bone disorders, immune disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arcccaaactarcaaaartraccraacacrccaacaaccrcrrarcccarrarcaaa
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Pred. No. 1.8e-163;
0; Mismatches 6; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 882 BP; 288 A; 150 C; 198 G; 245 T; 0 U; 1 Other;
                                            "Protein kinase 14275"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Fig 1A; 98pp; English.
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99.1%;
                                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                              13-APR-2001; 2001WO-US012188
                                                                                                                                                                                                                                                                           13-APR-2000; 2000US-0196910P
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                                                                                                                                                                                                                                                                                                                                                                     Kapeller-Libermann R;
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-034355/04.
P-PSDB; AAG78547.
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Best Local Similarity
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complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase expression and activity. Diseases related to down regulate kinase activity. Diseases related to kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune immune disorders, camplications of organ transplantation, myocardial infarction, stress related disorders, chronic inflammatory bowel disease, chornic inflammatory pelvic disease, multiple sclerosis, aschma, osteoarthritis, disorders in thinitis, autoimmunity, diabetes, cancers and reproductive
                                                                                                                                                                                                                                                                                                                                                                                      68.08;
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nes 643; Conservative
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Sequence 911 BP; 293 A; 182 C; 178 G; 258 T; 0 U; 0 Other;

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                                  285 AAATGGAGTTGGTGATGGAGTGATCAAAAGGGTATTATGGCAAACACTTCAAGGTTCTAA
                                               TTTCTGTCATATACATAACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAAC
                                                                                                          TAAGGAAGGAATAATCAAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGAGA
                                                                                                                                               TGCCTACACCGATTATGTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGA
                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                           825 AACCIGITCCCAACTCCTGGAGGCTCCTAGTTTGATTCTTTTCAAGAGGCCCGAAATTAA
                       ;
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                                                                                                                                                                                                                                                          AACACTAGGAAAATTAATCCCAAGACATCAATCAATCTTTAAAAGTAACGGGT"
   Length 911;
                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           885 AAGAAAAGCACGTAATGAAGGAAGAAACAGAAGACGCCAACAG
Score 643; DB 4; Le
Pred. No. 7.9e-163;
    100.0%; Pred. No.
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The invention relates to a compound comprising a sequence comprising 8-80 (MAP/microtubule affinity-regulating kinase 3), that specifically hybridises with the mucleic acid encoding MARK3 and inhibits expression of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a composition comprising the compound and a carrier or diluent, inhibiting suspected of having a disease or condition associated with MARK3 and suspected of having a disease or condition associated with MARK3 and useful for preparing a composition for treating hyperproliferative disorder, particularly cancer and neurodegenerative diseases e.g. Alzheimer's disease. The present sequence is a MARK3 associated cDNA included in the figures but not mentioned anywhere else in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           404
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                                                                                                                                                                                                                                                                                                                                                         New antisense compound targeted to a nucleic acid molecule encoding microtubule-affinity-regulating kinases (MARK3), useful for modulating expression of MARK3 or for treating cancer or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 AAATGGAGTTGCTGATGGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345 TITCTGTCATATACATAACTGTATTCACAGAGATATAAAAACCTGAAAATATTCTAATAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTCTGTCATATACATAACTGTATTCACAGAGATATAAAAACCTGAAAATATTCTAATAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAAGCAAGGAATAATCAAGATTTGTGACTTCGGGTTTGCACAAATTCTGATTCCAGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCCTACACCGATTATGTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TACTCAGTATGGTTCTTCAGTCGATATATGGGCTATTGGTTGTTTTTTGCAGAGCTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.0%; Score 643; DB 12; Length 911;
100.0%; Pred. No. 7.9e-163;
Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 911 BP; 293 A; 182 C; 178 G; 258 T; 0 U; 0 Other;
                                           cancer;
             Human, ss; antisense gene therapy; MARK3;
MAP/microtubule affinity-regulating kinase 3; cs
Alzheimer's disease; neurodegenerative disorde;
                                                               hyperproliferative disorder; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 2; 233pp; English.
                                                                                                                                                                                                                                                                                     Dobie KW;
                                                                                                                                                                                                                    17-JUN-2002; 2002US-00174319.
                                                                                                                                                                                     17-JUN-2002; 2002US-00174319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 643; Conservative
                                                                                                                                                                                                                                                    (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                              Ward DT, Freier SM,
                                                                                                                                                                                                                                                                                                                WPI; 2004-052188/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                         US2003232771-A1.
                                                                                                                                                                                                                                                                                                                                P-PSDB; ADI29249
                                                                                           Homo sapiens.
                                                                                                                                                       18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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644

585 GACAGGCCACTGTGGCCTGGAAATCAGATGTGGACCAACTTTATCTGATAATCAG

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Human MARK3-associated cDNA #37

(first entry)

22-APR-2004

ADI29367;

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ID ADI;
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ADI29367 standard; cDNA; 911

RESULT 12

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GAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACATCCAAATCTTGTGAA 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTGCTATGGCAAACCCTTCAAGCCCTTAACTTCTGTCACAAGCACAATTGTATTCATCG 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        658 arieccricaacaricaariccrearicacecreacererececeacerecreseres 717
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                          myocardial infarction, failure, oxidative-
disorders, complications of organ transplantation, myocardial infarction immune disorders, cardiomyopathies, strokes, renal failure, oxidativestress related disorders, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive disorders
                                                                                                                                                                                                                                                                                                                                                                                                    cercarcaaggrancagaagaagaagaagargarcarcragrringagracraraarca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 TGGATTTGCACGAATTCTAATTCCAGGAGACGCCTACACAGACTATGTTGCCACCAGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACACTTTTAAATGAGCTGGAAAGBAACCCAAATGGAGTTGCTGATGGAGGTGATCAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGIATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACATAACTGTATTCACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGGTTTGCACAAATTCTGATTCCAGGAGATGCCTACACCGATTATGTAGCTACGAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGTTCTTCAGTCGATATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     615 AGATGTGGACCCAACTTTATCTGATAATCAGAACACTAGGAAAATTAATCCCAAGACATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                675 ATCAATCTTTAAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAAGACAT
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                                                                                                                                                                                                                                                          Score 559.2; DB 4; Length 2615; Pred. No. 4.6e-140; Mismatches 143; Indels 3;
                                                                                                                                                                                                            Sequence 2615 BP; 742 A; 580 C; 585 G; 708 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGACGCCAACAGGTACTTCCGCT 938
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                                                                                                                                                                                                                                                                59.2%;
                                                                                                                                                                                                                                                                                        Local Similarity 81.8
ses 658; Conservative
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                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                          480
                                                                                                                                                                                                                                                                                                                540
                                                                                                                                                                                                                                                                                                                                                                                                    AACCTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTCTTTTCAAGAGGCCCAAATTAA 600
                                                        704
                                                                                                      420
                                                                                                                                                         764
                                                                                                                                                                                                                                                             824
                                                                                                                                                                                                                                                                                                                                                                   AACCTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTCTTTTCAAGAGGCCCAAATTAA 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic; immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic; dermatological; antidiabetic; antiinfertility; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease
                                                                                TGGCATCAGTATACCTGAGCCAGAAGACATGGAAACTCTTGAGGAAAAGTTCTCAGATGT
                                                     AACACTAGGAAAATTAATCCCAAGACATCAATCAATCTTTAAAAGTAACGGGTTTTTCCA
                                                                                                                                                         TGGCATCAGTATACCTGAGCCAGAAGACATGGAAACTCTTGAGGAAAAGTTCTCAGATGT
                                                                                                                                                                                                                                                                TCATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACATT
                                                                                                                                                                                                                                                                                             TCATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGAAAAGCACGTAATGAAGGAAGAACAGAAGACGCCCAACAG 927
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238 GGATGTAAAACCTGAAAAGGTCCTAATAACCAAGGGATGATAAAGATTTGTGACTT 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MDDT; human; disease detection and treatment molecule polypeptide; anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV; haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic; gene therapy; protein replacement therapy; cell proliferative disorder; cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma; anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS; Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
                                                              CGGGTTTGCACAAATTCTGATTCCAGGAGATGCCTACACCGATTATGTAGCTACGAGATG
                                                                                  GTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGTTCTTCAGTCGATATATG
                                                                                                                                               GGCTATTGGTTTTTTGCAGAGCTCCTGACAGGCCAGCCACTGTGGCCTGGAAAATC
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2001US-0280067P.
2001US-0280068P.
2001US-0291280P.
2001US-0291849P.
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29-MAR-2001;
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16-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense compound targeted to a nucleic acid molecule encoding microtubule-affinity-regulating kinases (MARK3), useful for modulating expression of MARK3 or for treating cancer or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 IGECTATGGCAAACCCTTCAAGCCTTAACTTCTGTCACAAGCACAATTGTATTCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 GAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACATCCAAATCTTGTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      315 CGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACATAACTGTATTCACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                        Mouse; ss; antisense gene therapy; MARK3; MAP/microtubule affinity-regulating kinase 3; c Alzheimer's disease; neurodegenerative disorde; hyperproliferative disorder; cytostatic.
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Pred. No. 4.6e-140;
); Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Fig 2; 233pp; English.
                                                                           Mouse MARK3-associated cDNA #12.
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Best Local Similarity 81.8%;
Matches 658; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                  Ward DT, Freier SM,
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                                                                                                                                                                                                                 US2003232771-A1.
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                                              22-APR-2004
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                 ADI29368;
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PR 19-UNW-2010; 2001018-0299428P.

PR 20-UNW-2001; 2001018-0299428P.

PR 20-UNW-2001; 2001018-0399428P.

PR 20-UNW-2001; 2001018-039940016.

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(INCY-) INCYTE GENOMICS INC.

PY Dagle C. P. A Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;

PI Daugherty SC, Dam TC, Liwis SA, Chen AJ, Panzer SR, Harris B;

PI Daugherty SC, Dam TC, Liwis SA, Chen AJ, Panzer SR, Harris B;

PI Plores V, Marwaha R, Lo A, Lan RY, Urashka ME;

XX WPI; 2003-058431/05.

DR WPI; 2003-058431/05.

DR WPI; 2003-058431/05.

DR WPI; 2003-058431/05.

DR WPI; 2003-058431/05.

TY POPULCHECKIGE, MEECHI for diagnosing, treating or preventing cancers or hepatitis.

TY Population of sarcoma), anemia, Crohn's disease, AIDS, Osteoporosis or hepatitis.

Claim 1; SEQ ID NO 240; 339pp + Sequence Listing; English.

XX This invention describes a novel disease detection and treatment molecule or hepatitis.

CC and any opeptied (MDDT) which has anti-inflammatory, immunosuppressive, osteopathic, cytostatic, anti-inflammatory, immunosuppressive, osteopathic, antipooriatic and hepatoropic activity. The polymoclectides are diseases or conditions. These polypeptides or the invention can be used for gene therapy, cortical array useful for diagnosing, treating or preventing cell continual. Jymphoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma, melanoma,
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                                                                         1 ATGGAAAAGTATGAAAAATTAGCTAAGACTGGAGAAAGGGTCTTATGGGGTTGTATTCAAA 60
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/ Match 57.5%; Score 543.2; DB 8; Length 1281; Local Similarity 99.5%; Pred. No. 7.1e-136; Les 545; Conservative 0; Mismatches 3; Indels 0;
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AX39997 Sequence
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AX12442 Ciona int
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AR21995 Sequence
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AR029045 Oryccolag
U35146 Homo sapien
CR407462 Gallus ga
BC083590 Rattus no
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Donoho,G., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B. and Sands,A.T.
Human kinase proteins and polynucleotides encoding the same
Patent: US 6716616-A 11 06-APR-2004;
Location/Qualifiers
1. 945
/organism="unknown"
                                                                                                                                                                                                                                                                                                                        linear PAT 15-MAY-2004
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AR492168 Sequence
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Sequence 11 from patent US 6716616.
AR492170.1 GI:47260680
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AX107712
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CQ14922
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                 GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT
                                                        GTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGTTCT
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Human kinase proteins and polymucleotides encoding
Patent: WO 0123579-A 11 05-APR-2001;
Lexicon Genetics Incorporated (US)
Location/Qualifiers
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/organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 11 from Patent W00123579.
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                                   1 AIGGAAAAGTAIGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA
                         1 ATGGAAAAGTATGAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA
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ilarity 100.0%; Pred. No. 1.7e-205;
Conservative 0; Mismatches 0;
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Sequence 5 from patent US 6716616.
AR492167
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AR492167
LOCUS
DEFINITION
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		Sands,A.T. Human kinase proteins and polynucleotides encoding the same Patent: WO 0123579-A 5 05-APR-2001; Lexicon Genetics Incorporated (US) Location/Qualifiers	/originsma="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	Query Match 98.3%; Score 929; DB 6; Length 972; Best Local Similarity 100.0%; Pred. No. 7.6e-202; Matches 929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Oy 1 AIGGAAAAGIAIGAAAAATIAGCTAAGACIGGAGAAGGGICTIAIGGGGITGTAITCAAA 60 Db 1 AIGGAAAAGIAIGAAAAAIIAGCTAAGACIGGAGAAGGGICTIAIGGGGIIGIAIIIIIIIIII	Oy 61 TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAATTTGTGGAATCTGAAGAT 120	Oy 121 GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAAACT 180	Qy 181 CCAAATCTTGFGAACCTCATCGAGGTGTTCAGGAAAAAGGAAAATGCATTTAGTTTTT 240 Db 181 CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAAGGAAAATGCATTTAGTTTTT 240	Qy 241 GAATACTGTGATCACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT 300 	Qy 301 GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360	Qy 361 AACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGGAATAATC 420	Qy 421 AAGATTTGTGACTTTGCACAAATTCTGATTCCAGGAGATGCTACACGGATTAT 480 Db 421 AAGATTTGTGACTTTGCACAAATTCTGATTCCAGGAGATGCTACACCGATTAT 480	Qy 481 GTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGAGATACTCAGTATGGTTCT 540
VERSION AR492167.1 GI:47260677 KEYWORDS SOURCE ORGANISM Unclassified. Unclassified. Unclassified. Unclassified. TITLE AUTHORS Donobo,G., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B. AUTHORS AUTHORS AUG SANGE,A.T. TITLE JOURNAL Patent: US 6716616-A 5 06-APR-2004; Location/Qualifiers Source /Organism="unknown" /mol_type="genomic DNA"	Query Match 98.3%; Score 929; DB 6; Length 972; Best Local Similarity 100.0%; Pred. No. 7.6e-202; 7.6e-202; Matches 929; Conservative 0; Mismatches 0; Indels 0; 0; Qy 1 ATGGAAAAGTATGAAAAATTAGCTAAGACTGGAAAAGGGTTCTATGAGGTTCTATTCAAA 60 Db 1 ATGGAAAAAGTATGAAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTCTATTCAAA 60 Co. 61 TGCAGAAAAAATTAGAAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTCTATTCAAA 60 Co.		OY 181 CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAGGAAAATGCATTTAGTTTT 240 DD 181 CCAAATCTTGTGAACCTCATCGAGGTGTTCAGGAGAAAAAGGAAATGCATTTAGTTTT 240	Qy 24.1 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAA	OY 301 GGAGTGATCAAAAGCGTATTATGGCAAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360	OY 361 AACTGTATTCACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATC 420 	Qy 421 AAGAITTCTGACTTTGGACTTTGCACAAATTCTGATTCCAGGAGATGCCTACACCGATTAT 480 Db 421 AAGAITTGTGACTTTGCACAAATTCTGATTCCAGGAGATGCCTACACCGATTAT 480	Oy 481 GTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGGTTCT 540	OY 541 TCAGTCGATATATGGGCTATTGGTTGTTTTTGCAGAGCTCCTGACAGGCCAGCCA	OY 601 TGGCCTGGAAARTCAGATGTGGACCAACTTTATCTGATAATCAGAACACTAGGAAAATTA 660	OY 661 ATCCCAAGACATCAATCTTTAAAAGTAACGGGTTTTTCCATGGCATCAGTATACCT 720	Qy 721 GAGCCAGAAGACATGGAACTCTTGAGGAAAAGTTCTCAGATGTTCATCCTGTGGCTCTG 780 Db 721 GAGCCAGAAGACATGGAAAACTCTTCAGGAAAAGTTCTCAGATGTTCATCCTGTGGCTCTG 780	AACTTCATGAAGGGTGTCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTC

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Plowman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R., Flanagan,P. and Clary,D.S.
Novel human protein kinases and protein kinase-like enzymes Patent: WO 0138503-A 25 31-MAY-2001;
Sugeh, Inc. (US)
Location/Qualifiers
1. .1083
971 AACTCCTGGAGAGCTCCTACTTTGATTCTTTTCAAGAGGCCCAAATTAAAAGAAAAGCAC 1030
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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91.3%; Score 863; DB 6; 1
Best Local Similarity 94.5%; Pred. No. 9.2e-187;
Matches 927; Conservative 0; Mismatches 0;
                                                  DNA
                                 896 GTAATGAAGGAAGAACAGAAGACGCCAACAG 927
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                                                                                                                                 Sequence 25 from Patent W00138503.
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/organism="Homo sapiens"
/organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: LI:058298.1:2001JAN12"
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 Molecules for diagnostics and therapeutics Patent: WO 02079471-A 6 10-0CT-2002; Incyte Genomics, Inc. (US)
                                                                                                                                                                    91.9%; Score 868.8; DB 6;
99.2%; Pred. No. 4.1e-188;
tive 0; Mismatches 2;
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ATGAATCCAGATGACAGATTAACCTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTCT 960
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                                                                                                                   88.8%; Score 839; DB 6; L
llarity 90.8%; Pred. No. 2.8e-181;
Conservative 0; Mismatches 0;
            1. .1041
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Zambrowicz, B.

us-10-766-691-11.rge

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	Qy 651 650 Db 661 GGGTTTCGCCATGTTGACCAGGCTGGTCTCGAACTCTTGACGTCAAGTGATCCACCTGCC 720	OY 651	OY 685 AAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCAGAAGACATGGAAACTCTT 744	Qy 745 GAGGAAAAGTTCTCAGATGTTCATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAG 804	OY 805 AIGAAICCAGAIGACAGAITAACCIGIICCCAACICCIGGAGGCICCIACITIGAITCI 864	OY 865 TITCAAGAGGCCCAAAITAAAAGAAAAGCACGTAATGAAGGAAGAAACAGAAGACGCCAA 924 	Cy 925 CAGGT 929	RESULT 11	- F	AX107714 AX107714.1 GI:1392319	Homo sapiens (human) SM Homo sapiens Eukaryota; Metazoa; Chordata;	rimates; Catarrhini; Hominidae; Homo, Nehls,M., Friedrich,G., Zambrowic	TITLE SANGE, ALT ALTA SANGE DISTRIBUTED SOLVEN TO STATE SANGE STATES AND SANGE STATES AND SANGE	source 11068 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	y Mat Loca	Matches 929	DD 1 ATGGAAAAGTATGAAAATTAGCTAAGAGTGAGAAAGGGTCTTATGGGGTTGTATTCAAA 60 QY 61 TGCAGAAACAAAACTCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 0179488-A 3 25-OCT-2001;
Millennium Pharmaceuticals, Inc. (US)
                                                                                                                                                                  Score 647; DB 6; L
Pred. No. 2.3e-137;
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    .687
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Pred. No. 2.2e-137;
0; Mismatches 5;
                                   Kapeller-Libermann, R. 14257, protein kinase molecules and uses Patent: WO 0179488-A 1 25-OCT-2001, Millennium Pharmaceuticals, Inc. (US) Location/Qualifiers
                                                                                                                                                                                                                                                                      /note="unnamed protein product"
                                                                                                                                                      1. .882
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                  /codon start=1
/protein id="CAD12176.1"
/db_xref="GI:17045994"
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99.2%;
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Matches 650; Conserv
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RESULT 14

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PAT 13-JAN-2001
                                                                             Murinae gen. sp.
Murinae gen. sp.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae.
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                                                                                                                                                     Plowman,G.D., Martinez,R., Whyte,D. and Sudersanam,S. Protein kinases
Patent: WO 0073469-A 49 07-DEC-2000;
Sugen, Inc. (US)
             DNA

    .2615
    /organism="Murinae gen. sp./mol type="unassigned DNA" /db_xref="taxon:39108"

          AX056405 2615 bp
Sequence 49 from Patent WO0073469.
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AX056405.1 GI:12229112
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                             Plowman,G.D., Martinez,R., Whyte,D. and Sudersanam,S. Protein kinases
Patent: WO 0073469-A 48 07-DEC-2000;
Sugen, Inc. (US)
                                                                                                                                                                                                                                                                                                                      Query Match 68.0%; Score 643; DB 6; Length 911; Best Local Similarity 100.0%; Pred. No. 1.8e-136; Matches 643; Conservative 0; Mismatches 0; Indels
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                   DNA
                                                                                                                                                                                                                                   1. .911
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
             Sequence 48 from Patent WO0073469.
AX056404
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                                                                                     Homo sapiens (human)
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Search completed: April 21, 2005, 23:37:14 Job time: 4113.75 secs

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The present sequence is novel human protein (NHP) known as human kinase. The human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in adjagnostic assays, for the identification of other cellular gene products related to human kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                         2105692 seqs, 386760381 residues
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                                           OM protein - protein search, using sw model
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AAE00494
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AAE00491
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Gapop 10.0 , Gapext 0.5
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geneseqp1990s:*
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length: 2000000000
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Adi57214 Human NK	Adi57236 CDK3 domi	Aau03524 Human pro	Aay70125 Rat lost	Rat 1	Abm83922 Human dia	Abu05290 Human dia	Novel	Adi29252 Human MAR	Human	Adj68738 Human 1	Adi57200 Human CDK	Adi57237 CDK3 domi	Aam39276 Human po]	Aam41062 Human po	Aaw95689 Homo sapi	Aaw85028 CDK2-gree	Aaw85029 Green flu	Abg06142 Novel hum	Add21390 Human cyc	
ADI57214	AD157236	AAU03524	AAY70125	AAY70124	ABM83922	ABU05290	AAB65645	AD129252	ADF45039	ADJ68738	ADI57200	AD157237	AAM39276 .	AAM41062	AAW95689	AAW85028	AAW85029	ABG06142	ADD21390	
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455	455	591	457	505	562	154	534	534	305	305	305	305	333	352	298	544	544	224	298	
47.2	47.2	47.2	45.9	45.9	43.6	42.9	39.5	39.5	35.0	35.0	35.0	35.0	35.0	34.5	34.3	34.3	34.3	34.2	34.2	
784.5	784.5	784.5	763.5	763.5	725	712.5	959	959	581	581	581	581	581	574	570	570	570	569	569	
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4.5	

ALIGNMENTS

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New isolated human kinase polynucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases.
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                                                                                                                                                                                        Human; kinase; gene therapy; bioreactor; mental disorder; biological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Friedrich G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 33-34; 38pp; English.
AAE00495 standard; protein; 315 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Turner CA, Nehls M,
                                                                                                                                                                                                                                                                                                                                                                                                      27-SEP-2000; 2000WO-US026621.
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                                                                                             (first entry)
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N-PSDB; AAD03817.
                                                                                                                                         Human kinase #6.
                                                                                                                                                                                                                                                                                                         NO200123579-A1
                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-SEP-1999;
                                                                                             19-JUN-2001
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Sands AT;
                                              AAE00495;
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probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP products are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression
                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                           SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGISIP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCIHRDIKPENILITKQGIIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTQYGS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRLTCSQLLESSYFDSFQEAQIKRKARN 300
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                                                                                                                                                                                                                                                            1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
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                                                                                                                                                                                                                                 Gaps
     The labelled NHP
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                                                                                                                                                                                                Length 315;
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                                                                                                                                                                                            100.0%; Score 1662; DB 4;
100.0%; Pred. No. 1.5e-168;
ilve: 0; Mismatches 0;
 disorders. NHP oligonucleotides
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Best Local Similarity 100.0
Matches 315; Conservative
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                                                                                                                                                                Sequence 315 AA;
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AAE19152 standard; protein; 342 21-MAY-2002 (first entry) AAE19152 RESULT 2
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Human kinase polypeptide (PKIN-10).

Human; kinase polypeptide; PKIN-10; gene therapy; Addison's disease; leukaemia; immune disorder; lymphoma; melanoma; developmental disorder; acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension, asthma; Crohn's disease; rheumatoid arthitis; burstis; atherosclerosis; cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer; cholestasis; cardious, cardiousder, sorder, Niemann-Pick's disease; lipid disorder; fatty liver; Gaucher's disease; myocardial infarction; drug screening; transgenic animal; antiinflammatory; hepatotropic; drug screening; transgenic ani hypotensive; anti-HIV; enzyme.

Homo sapiens

/note= "Eukaryotic protein kinase domain' Location/Qualifiers 4. .286 Domain

WO200208399-A2

31-JAN-2002

20-JUL-2001; 2001WO-US023092

EGRNRRRQ--QVLPL 313

301

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The present invention relates to an isolated human kinase polypeptide (PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is useful for diagnosing, treating and preventing cancer (e.g., Deukaemia, Immunoma, melanoma), an immune disorder (e.g., acquired immunodeficiency syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's cardiovascular disorder (e.g., atherost), angerlonental disorder (e.g. bursitis, cirrhosis, hepatitis, psoriasis, Cushing's syndrome), a cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial infarction), and a lipid disorder (e.g., fatty liver, cholestasis, Gaucher's disease, Niemann-Pick's disease). PKIN is useful in a number of chug screening techniques and to analyse the proteome of a tissue or cell type. PKIN is useful for creating knockin humanised animals or transgenic animals to model human diseases, in sometic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting confiferences in the chromosomal location due to translocation, inversion, croposes for mapping naturally occurring genomic sequences. PKIN is useful crechnologies, in dipstick, pin, multiformat enzyme clinked immunosorbent (ELISA)-like assays and in microarrays utilising the core present sequence is human PKIN-10
                                                                                                                                                                                                                                                                                                                                                            New human kinase polypeptide, useful in diagnosis, prevention and treatment of cancer, immune disorder, growth and developmental disorder, cardiovascular disorder and lipid disorder.
                                                                                                                                                            Thornton M, Yue H, Khan FA, Gururajan R, Hafalia AJA, Walia NK; Patterson C, Ramkumar J, Gandhi AR, Policky JL, Baughn MR; Tribouley CM, Bandman O, Nguyen DB, Lu Y, Burford N, Lal P, Ding Yao MG, Elliott VS, Recipon SA, Kearney L, Lu DAM, Greenwald SR; Tang YT, Xu Y, Walsh RT, Gietzen KJ, Yang J, Hillman JL:
                                                                                                                                                                                                                                      Lu DAM, Green
7, Hillman JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 147-148; 196pp; English
; 2000US-0220038P.
; 2000US-0222112P.
; 2000US-0222831P.
; 2000US-0224729P.
                                                                                                         GENOMICS INC.
                                                                                                                                                                                                                                                                                                  2002-206083/26.
                                                                                                                             THORNTON M.
                                                                                                                                                                                                                                                                                              WPI; 2002-ZUBUC,...
N-PSDB; AAD30557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 342 AA;
                                                                                                         INCYTE
                                     04-AUG-2000;
11-AUG-2000;
                      28-JUL-2000;
                                                                                                                             (THOR/)
                                                                                                         INCX-)
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120 120 180 300 9 9 61 PNLVNLIEVFRRRKKKKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLMQTLQALNFCHIH 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGOVVAVKKFVESEDDPVVKKIALREIRMLKOLKH 61 PNLVNLIEVFRRRRRMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 121 NCIHRDIKPENILITKOGIIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTQYGS 121 NCIHRDIKPENILITKQGIIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTQYGS SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGISIP 181 SVDIWAIGCVFAELLIGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGISIP **EPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRLTCSQLLESSYFDSFQEAQIKRKARN** Gaps 5; Length 342; Indels 9; DB 5; 4.9e-166; ö ; Score 1639; DB ; Pred. No. 4.9e-1; Mismatches 98.6%; Best Local Similarity 99.0 Matches 312; Conservative Query Match 181 241 ð 셤 ò g ò 셤 ઠ g 셤 ò

SVDIWAIGCVFAELLIGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGISIP 240

EPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRLTCSQLLESSYFDSFQEAQIKRKARN

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121 NCIHRDIKPENILITKQGIIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTQYGS SVDIWAIGCVFAELLIGOPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGISIP

NCIHRDIKPENILITKOGIIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTQYGS

121

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셤 8 Б

181 181

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The present sequence is novel human protein (NHP) known as human kinase.

The human kinases share structural similarity with animal kinases, more particularly series or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations of fective in the treatment of Symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the identification of other cellular gene products compounds that are useful for treating mental, biological or medical disorders. NHP oligonucleotides are used as probes. The labelled NHP probes are useful for screening human genomic library for identifying colymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated human kinase polynucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zambrowicz B;
                                                                                                                                                                                                                                                         Human; kinase; gene therapy; bioreactor; mental disorder;
biological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nehls M, Friedrich G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 30; 38pp; English.
                                                                                                                 AAE00492 standard; protein; 324 AA.
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301 EGRNRRRQQNQLLPL 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-266166/27.
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                                                                                                                                                                                                                                  Human kinase #3
                                                                                                                                                                                                                                                                                                                                                                   40200123579-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-SEP-1999;
                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Sands AT;
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                                                                                               AAE00492
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The present sequence is novel human protein (NHP) known as human kinase.

The human kinases share structural similarity with animal kinases, more particularly serine or threading by the particularly serine or threading by the particularly serine or the construction by the construction of mutant human kinases. Human kinase cDNA is useful for the detection of mutant human kinases. Human kinase cDNA is useful for the detection of symptomatic or phenotypic manifestations of fetctive in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in agencies that can products related to human kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical disorders. NHP oligonucleotides are used as probes. The labelled NHP compounds that as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP
241 EPEDMETLEEKFSDVHPVALNFMKGCLKANPDDRLTCSQLLESSYFDSFQEAQIKRKARN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated human kinase polynucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zambrowicz B;
                                                                                                                                                                                                                                                                                                                                   Human; kinase; gene therapy; bioreactor; mental disorder;
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                                                                                                                                                                                  AAE00494 standard; protein; 347 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Turner CA, Nehls M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LEXI-) LEXICON GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2000; 2000WO-US026621
                                                                                                                                                                                                                                                          (first entry)
                                                                              EGRNRRROOV 310
                                                   EGRNRRRQQV 310
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                                                                                                                                                                                                                                                                                                                                                        biological disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAD03816.
                                                                                                                                                                                                                                                                                              Human kinase #5.
                                                                                                                                                                                                                                                                                                                                                                                                                             WO200123579-A1.
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                          19-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Donoho G,
                                                                                                                                                                                                                     AAE00494;
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0; Gaps

0; Indels

98.6%; Score 1638; DB 4; L 100.0%; Pred. No. 5.8e-166; ive 0; Mismatches 0;

Conservative

Local Similarity les 310; Conserv

Query Match Best Loca Matches

Length 324;

9

PNLVNLIEVFRRKRKWHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120

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1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGOVVAVKKFVESEDDPVVKKIALREIRMLKQLKH

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217
                                                                                                                                                                                                    NCIHRDIKPENILITKQGIIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTQYGS 180
                                                                                                                                                                                                                                                                                                                                            268
                                                                                                                                                                                      PNLVNLIEVFRRKRKMHLVFEYCDHTLINELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                                                                                                                                                                                      SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
                                                                                                                                                                                                                                                                                                                                                        241 VASQSAGITGKLIPRHQSIFKSNGFFHGISIPFPEDMETLEEKFSDVHPVALNFWKGCLK 300
                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding human kinase polypeptides, useful for preventing diagnosing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections.
                                                                                                                                                    products are used to genetically engineer cells in vivo that functions bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression
                                                                                                                                       1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                                                                                                                                                                                                                                        -----GKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, protein kinase, PTK, STK, cancer; cardiovascular disease;
metabolic disorder; immune related disease; neurological disorder;
neurodegenerative disorder; inflammatory disorder; infectious disease;
                                                                                                                  Gaps
                                                                                                                  32;
                                                                                          Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                      Martinez R;
                                                                                                                                                                                                                                                                                                                                                                                        MNPDDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQQVLPLKS 315
                                                                                      Score 1636; DB 4; Length 347
Pred. No. 1e-165;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                        SVDIWAIGCVFAELLTGOPLWPGKSDVDQLYLIRTL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G, Sudarsanam S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU03525 standard; protein; 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Manning
                                                                                    98.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                 Best Local Similarity 90.8
Matches 315; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human protein kinase #25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reproductive disorder.
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Clary D;
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                                                              Sequence 347 AA;
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                                                                                                                                                                                                                                                                                                                                                                                        269
                                                                                       Query Match
                                                                                                                                                                                       61
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AAU03501-AAU03557 represent novel human protein kinases #1-57. The novel protein kinases have been identified as members of the tyrosine or serine thrace (PTK and STK) families. The polymucleotides control than the protein kinases and the polymptides may be used in the protein kinases and the polymptides may be used in the prevention, diagnosis and treatment of diseases associated with cancers (especially cancers of haematopicitic origin), cardiovascular cancers (especially cancers of haematopicitic origin), cardiovascular disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), immune related diseases (e.g. rheumatoid arthritis), neurological disease (e.g. schizophrenia), neurodegenerative disorders (e.g. diabetes), parkinson's disease), inflammatory disorders (e.g. asthma), infectious disease (e.g. HIV) and reproductive disorders (e.g. infertility).

Additionally, polymucleotides encoding protein kinases may be used for gene therapy and as DNA probes in disquestic assays. The protein kinase polypeptides may be used as antiqens in the production of antibodies against the protein kinases and in assays to identify modulators of protein kinase expression and activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 PNL/NLIEVFRRKRKM/HLVFEYCDHT/LINELERNFNGVADGVIKSVLMQTLQALNFCHIH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 RHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRLTCSQLLE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PNLVNLIEVFRKRKRKMHLVFEYCDHTLINELERNPNGVADGVIKSVLWQTLQALNFCHIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 TRWYRAPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                                             Length 360;
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biological disorder..
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Pred. No. 7.3e-164;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSYFDSFQEAQIKRKARNEGRNRRRQ--QVLPL 313
 Claim 7; Fig 2; 433pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE00491 standard; protein; 356
                                                                                                                                                                                                                                                                                                                                                                                                         97.48;
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 93.4°
Matches 311; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                    Sequence 360 AA;
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The present sequence inverting in the present sequence in the present sequence in the present sequence in the present sequence in the present sequence in the present sequence in the present sequence in the detection of mutant human kinases. Human kinases, more disease, and also as a therapeutic. It is useful for screening drugs of disease, and also as a therapeutic. It is useful for screening drugs of perturbing the normal function of NHP in the body. The NHP mucleotide sequences are useful for generation of antibodies, as reagents in disponsite assays, for the identification of other cellular gene products celated to human kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical disponders. NHP oligonucleotides are used as probes. The labelled NHP probes are useful for screening human genomic library for identifying colymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in disponsities and pharmacogenomics. Nucleotide construct encoding NHP to the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression
                                                                                                                                                                                                                                                                                                                                                                  sequence is novel human protein (NHP) known as human kinase
                                                                                                                                                                                                              New isolated human kinase polymucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases.
                                                                    ä
                                                                    Zambrowicz
                                                                    Turner CA, Nehls M, Friedrich G,
                                                                                                                                                                                                                                                                                                                  Disclosure; Page 28-29; 38pp; English.
                    (LEXI-) LEXICON GENETICS INC
                                                                                                                                         2001-266166/27.
                                                                                                                                                                   N-PSDB; AAD03813
                                                                  Donoho G,
Sands AT;
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Sequence 356 AA; Query Match

ij 120 240 121 NCIHRDIKPENILITKQGIIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTQYGS 180 217 241 VASQSAGITGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFWKGCLK 300 PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLMQTLQALNFCHIH 120 180 9 9 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH NCIHRDIKPENILITKQGIIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTQYGS SVDIWAIGCVFAELLTGOPLWPGKSDVDOLYLIIRTL -----GKLI PRHQSI FKSNGFFHGI SI PEPEDMETLEEKFSDVHPVALNFMKGCLK 97.0%; Score 1612; DB 4; Length 356; 90.6%; Pred. No. 4e-163; iive 0; Mismatches 0; Indels 32; Gaps MNPDDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQQV 310 MNPDDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQQV 342 Best Local Similarity 90.6 Matches 310; Conservative 61 61 121 181 181 569 301 218 ઠે g Š ò 셤 ò 윱 8 9 8 셤

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AAB65643 standard; protein; 296
                     AAB65643
AAB65643
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RESULT 7

YRAPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQ

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The present sequence is a novel protein kinase. The novel protein kinases and the nucleic acids that encode them may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase antagonists may also be used to down regulate kinase activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative-stress related disorders, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, proteins, rhinitis, autoimmunity, diabetes, cancers and reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ñ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 KIALREIRMLKOLKHPNIVNLIEVFRKKRKMHLVFEYCDHTLLNELERNPNGVADGVIKS 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 VLWQTLQALNPCHIHNCIHRDIKPENILITKQGIIKICDFGFAQILIPGDAYTDYVATRW 165
                                                                            Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic; immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic; dermatological; antidabetic; antiinfertility; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; autiliple sclerosis; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KIALREIRMLK-LKHPNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVSDGVIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 VLWQTLQALNFCHKHNCIHRDVKPENILITKQGMIKICDFGFARILIPGDAYDYVATRW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sudersanam S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurodegenerative diseases and/or cancers
                                       Novel protein kinase, SEQ ID NO: 170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Whyte D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Fig 1; 310pp; English.
                                                                                                                                                                                                                                                                                                                                                             26-MAY-2000; 2000WO-US014842.
                                                                                                                                                                                                                                                                                                                                                                                                    28-MAY-1999; 99US-0136503P
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plowman GD, Martinez R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 243; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 296 AA;
                                                                                                                                                                                                                                                                            WO200073469-A2
                                                                                                                                                                                                                                    fus musculus.
  27-MAR-2001
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New antisense compound targeted to a nucleic acid molecule encoding microtubule-affinity-regulating kinases (MARK3), useful for modulating expression of MARK3 or for treating cancer or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse; antisense gene therapy; MARK3;
MAP/microtubule affinity-regulating kinase 3; ca
Alzheimer's disease; neurodegenerative disorde;
hyperproliferative disorder; cytostatic.
                                   240 FESFQEDQMKRKARSEGRSRRRQQNQLLPL 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 170; 233pp; English
286 FDSFQEAQIKRKARNEGRNRRRQ--QVLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse MARK3-associated protein #12
                                                                                                                                                                                                                                       ADI29250 standard; protein; 296
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                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DT, Freier SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2004-052188/05.
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cancer;

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The invention relates to a compound comprising a sequence comprising 8-80 base pairs (bp) targeted to a nucleic acid encoding MARK3 (MAP/microtubule affinity-regularing kinase 3), that specifically hybridises with the nucleic acid encoding MARK3 and inhibits expression of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a composition comprising the compound and a carrier or diluent, inhibiting the expression of MARK3 in cells or tissues, treating an animal having or suspected of having a disease or condition associated with MARK3 and screening for an antisense compound. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disorder, particularly cancer and neurodegenerative diseases e.g. Alzheimer's disease. The present sequence is a MARK3 associated protein included in the figures but not mentioned anywhere else in the
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7 46 KIALREIRMLKQLKHPNLVNLIEVFRRKRKWHLVFEYCDHTLLNELERNPNGVADGVIKS 105 Gaps 3; 78.0%; Score 1296.5; DB 8; Length 296; 90.0%; Pred. No. 1.7e-129; ive 19; Mismatches 5; Indels 3; Indels Conservative Local Similarity tes 243; Conserv Query Match Best Loca Matches

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106 VLWQTLQALNFCHIHNCIHRDIKPENILITKQGIIKICDFGFAQILIPGDAYTDYVATRW 165
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1 KIALKEIRMLK-LKHPNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVSDGVIKS

g ò

59

71.5%; Score 1188.5; DB 5; Length 358;

Sequence 358 AA;

Query Match

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166 YRAPELLVGDTQYGSSYDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQ 225
                     The invention relates to an isolated polynucleotide (I) comprising one of administering to a manmalian subject a composition comprising deministering to a manmalian subject a composition comprising the protein (II) encoded by (I) (ABP62809-ABP631053) or an antibody (III) to (III).

(I), (II) and (III) are useful for diagnostic evaluation of disorders.

(I) is useful for gene therapy of diseases and (II) can be used for therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                              Human; vulnerary; dermatological; neuroprotective; nootropic; cancer; antiparkinsonian; immunostimulant; cytostatic; immunosuppressive; antidiabetic; antiallergic; gene therapy; wound healing; tissue repair; burn; central nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; immune disorder; autoimmune disorder; multiple sclerosis; diabetes; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzheimer's, Parkhison's, Huntington's, amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies.
                                                                        SIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRLTGSQLLESSY
                                                                                                 SIFRSNQFFRGISIPEPEDMETLEEKFSNVQPVALSFMKGCLKMNPDERLTCAQLLDSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID NO 391; 284pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asundi V, Zhou P, Xue AJ, Ren F, Zhai
Wang D, Liu C, Drmanac RT, Wehrman T;
                                                                                                                                                                      286 FDSFQEAQIKRKARNEGRNRRRQ--QVLPL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published pct sequences
                                                                                                                                                                                                                                                                                     Ź
                                                                                                                                                                                                                                                                                                                                                                                            Human polypeptide SEQ ID NO 391.
                                                                                                                                                                                                                                                                                 ABP62954 standard; protein; 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-AUG-2001; 2001WO-US027093.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-SEP-2000; 2000US-00654935.
                                                                                                                                                                                                                                                                                                                                                         (first entry)
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N-PSDB; ABQ93433.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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Zhao QA,
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WPI; 2001-032161/04.
N-PSDB; AAF44669.
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                                                                                                     Sequence 358 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                  239
                                                                         PNLVNLIEVFRRKRKRKMHLVFEYCDHTLINELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                NCIHRDIKPENILITKQGIIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTQYG 179
                                                                                                                        9
                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of cyclin-dependent kinase like 1 polypeptides or nucleic acids for modulating branching morphogenesis in a mammalian cell or for diagnosing a disease e.g. angiogenic, apoptotic or proliferation disorder in a
                                                                                                                                                                                                                                                                                                                                                                  human; cyclin-dependent kinase like 1; CDKL1; branching morphogenesis; branching morphogenesis modulator; angiogenic disorder; apoptotic disorder; proliferation disorder; chromosome 14.
                                                                                                                                                            MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                              SSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGISI
                                                                                                                                                                                       PEPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRLTCSQLLESSYFDSFQEAQIKRKAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AM;
                                                                                                                                                                                                                                                                                                                                                  Human cyclin-dependent kinase like 1 (CDKL1) protein SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HA, Koblizek II;
GM, Trowe T, Vogel
    8e-118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hai B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Habeck HA,
Stott GM,
Jin Y, Ha
        Pred. No. 8e-1
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plowman GD, Karim FD, Swimmer C,
Schulte-Merker S, Langheinrich U,
Odenthal JH, Scheel JK, Will TT,
70.5%; ***
                                                                                                                                                                                                                                                                                           ADO01538 standard; protein; 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-OCT-2002; 2002US-0420554P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-OCT-2003, 2003WO-US033483
                                                                                                                                                                                                                                                                                                                                (first entry)
                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EXEL-) EXELIXIS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-365563/34.
N-PSDB; ADO01535.
        Local Similarity
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NK 303
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                                                                                                                                                                                                                           NE 301
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                                                                         61
                                                                                                                                                  180
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a mammalian cell comprising contacting the cell with an agent that specifically binds a CDKL1 polypeptide or nucleic acid; and (3) a method for diagnosing a disease in a patient. The CDKL1 polypeptide or nucleic acid is useful for modulating branching morphogenesis in a mammalian cell. It is also useful for diagnosing a disease, e.g. angiogenic, apoptocic or proliferation disorder in a patient. The present sequence represents human CDKL1, which is used in the exemplification of the present invention. The human CDKL1 gene is located on chromosome 14, more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCIHRDIKPENILLITKQGIIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTQYG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGISI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, mouse; protein kinase; antiarthritic; antisclerotic; osteopathic; immunosuppressive; cardiant; renal; antinflammatory; antiasthmatic; dermatological; antidabetic; antiinfertility; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 PPVDVWAIGCVPAELLSGVPLWPGKSDVDQLYLIRKTLGDLIPRHQQVFSTNQYFSGVKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                            DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41;
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                                                                                                                                                                                                                                                                                                                                                                                                         71.2%; Score 1183.5; DB 8
71.8%; Pred. No. 2.8e-117;
iive 41; Mismatches 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB65642 standard; protein; 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 71.8
Matches 211; Conservative
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                                                                                                                                                                                                                                                                                  specifically to 14q22.1.
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The present sequence is a novel protein kinase. The novel protein kinases and the nucleic acids that encode them may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, complementary sequences may also be used as DNA probes in diagnostic complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies antagonists may also be used to down regulate kinase activity. Diseases related to kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, cardiomyopathies, strokes, renal failure, oxidative-stress related disorders, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, allowed the productive discase, renal failure, candictive disease, multiple sclerosis, asthma, osteoarthritis, allowed asthmistis, rhinitis, autoimmunity, diabetes, cancers and reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1149; DB 4; Length 247; Pred. No. 7.7e-114; 1; Mismatches 0; Indels 2
neurodegenerative diseases and/or cancers.
                                                  Claim 10; Fig 1; 310pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 98.6
Matches 217; Conservative
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96 NGVADGVIKSVLWQTLQALNFCHIHNCIHRDIKPENILITKQGIIKICDFGFAQILIPGD 155 1 NGVADGVIKSVLAGTLOALNFCHINCIHRDIKPENILITKQGIIKICDFGFAQILIFQD 61 AYTDYVATRWYRAPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIR 216 TLGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRL 156 AYTDYVATRWYRAPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLLIR TCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQONQLLPL 220 276 TCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQ--QVLPL 313 181 셤 g ઠ ò g ò В

215

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120

275

Human MARK3-associated protein #37 ADI29249 standard; protein; 247 (first entry) 22-APR-2004 ADI29249;

cancer; Human, antisense gene therapy, MARK3; MAP/Microcrubule affinity-regulating kinase 3; c Abheimer's disease, neurodegenerative disorde; hyperproliferative disorder; cytostatic.

US2003232771-A1. Homo sapiens

18-DEC-2003

17-JUN-2002; 2002US-00174319

17-JUN-2002; 2002US-00174319.

(ISIS-) ISIS PHARM INC.

Freier SM, Dobie KW; Ward DT,

Location/Qualifiers

Homo sapiens

Key

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The invention relates to a compound comprising a sequence comprising 8-80 base pairs (bp) targeted to a nucleic acid encoding MARK3 (MAP/Microtubule affinity-regulating kinase 3), that specifically hybridises with the nucleic acid encoding MARK3 and inhibits expression of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a composition comprising the compound and a carrier or diluent, inhibiting the expression of MARK3 in cells or tissues, treating an animal having or suspected of having a disease or condition associated with MARK3 and screening for an antisense compound. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disorder, particularly cancer and neurodegenerative diseases e.g. Alzheimer's disease. The present sequence is a MARK3 associated protein included in the figures but not mentioned anywhere else in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AYTDYVATRWYRAPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein kinase, enzyme; cytostatic; osteopathic; hepatotropic; antidabetic; neuroprotective; antiarthritic; dermatological; immunosuppressive; antianflammatory; antithyroid; antipsoriatic; ophthalmological; antiallergic; antiatchwroid; antiatherosclerotic; ophthalmological; antiallergic; antiatchmatic; antiatherosclerotic; immunomodulator; analgesic; cellular proliferative disorder; cancer; acute lymphoblastic leukaemia; Hodgkin's disease; acute lymphoblastic leukaemia; Hodgkin's disease; inflammatory; diabetes mellitus; osteoarthritis; asthma; cardiovascular disorder; osteoporosis; immune system disorder; cancer; cardiovascular disorder; hypertension; coronary artery disease; endothelial cell disorder; psoriasis.
                                                                                  New antisense compound targeted to a nucleic acid molecule encoding microtubule-affinity-regulating kinases (MARK3), useful for modulating expression of MARK3 or for treating cancer or Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96 NGVADGVIKSVLWQTLQALNFCHIHNCIHRDIKPENILITKQGIIKICDFGFAQILIPGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 TLGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 NGVADGVIKSVLWQTLQALNFCHINCIHRDIKPENILITKQGIIKICDFGFAQILIPGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 AYTDYVATRWYRAPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 247;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 TCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQQNQLLPL 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 TCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQ--QVLPL 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1149; DB 8;
Pred. No. 7.7e-114;
1; Mismatches 0;
                                                                                                                                                                        Disclosure; SEQ ID NO 169; 233pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human kinase 14257 amino acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG78547 standard; protein; 228 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 98.6%;
Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                  WPI; 2004-052188/05.
N-PSDB; ADI29367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 247 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-2002
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Gaps

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Length 228; Indels

Score 1140; DB 5; Pred. No. 6.3e-113;

68.6**%**; 98.2**%**;

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"tyrosine kinase phosphorylation site"
     "eukaryotic protein kinase domain"
                                       "N-myristoylation site"
                                                            /note= "N-myristoylation site"
                                                                                                                   188. .193
/note= "N-myristoylation site"
                     .26
re= "N-glycosylation site"
                                                                                                                                                                                                                                                                          Claim 1c; Fig 1A; 98pp; English.
                                                                                                                                                                                                        (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                  13-APR-2001; 2001WO-US012188
                                                                                                                                                                                             13-APR-2000; 2000US-0196910P
                                                                .134
                                                                                                                               .211
                                                                                                                                           .208
                                                                                                         180. .183
                                                       .102
                                                                                                                                                                                                                                                                cardiovascular disorders.
                                            .41
4. .218
/note= "
9. .15
                           note=
                                       note=
                                                  note=
                 note=
                                                                                                                                                                                                                   Kapeller-Libermann R;
                                                                                                                                                                                                                             WPI; 2002-034355/04.
N-PSDB; AAI64248.
                                                                                                                                                            WO200179488-A2
           Modified-site
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 Domain
                                                                                   Domain
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PNLVNLIEVFRRKRKMHLVFEYCDHALLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                                                                                                               PNLVNLIEVFRKRKKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                                                                                                                                                                                                      NCIHRDIKPENILITKQGIIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTQYGS 180
                                                                                                                                                                                                                                                                                                1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                               1 MGKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPIVKKIALREIRMLKQLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster polypeptide SEQ ID NO 16146.
                                                                                                                                                                                                                                                                                                                                                              SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLG 218
                                                                                                                                                                                                                                                                                                                                                                                        181 SVDIWAIGCVFAELLIGOPLWPGKSDVDOLYLIIRTIG 218
                                            2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB63118 standard; protein; 392 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
Query Match
Best Local Similarity 98.2
Matches 214; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Orosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABL07221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 392 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmaceutical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-2001.
                                                                                                                                                                               61
                                                                                                                                                                                                                                                                      121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated 14257 polypeptide and nucleic acid encoding it. The 14257 protein is a protein kinase that acts as a modulating agent in regularing a variety of cellular processes, including cell proliferation, differentiation, growth and division. The activity of the protein of the invention may be described as; cytostatic; osteopathic; hepatotropic; antidiabetic; neuroprotective; antiarthritic; hepatotropic; antidiabetic; natialleragic; antiarthritic; antipsoriatic; ophthalmological; antialleragic; antiarthritic; antiatherosclerotic; hypotensive; vasotropic; antiarthritic; canciented as nonectic; metabolic; immunomodulator and analgesic. The protein of the invention may act as a novel diagnostic target or therapeutic agent controlling certain disorders, for example kinase-associated or other controlling certain disorders. These may include cellular proliferative disorders such as cancers e.g. acute lymphoblastic leukemia or Hodgkin's disease. Other disorders include bone metabolism disorders such as
                                                                                                                                                                                                                                                                                                                                      /note= "kinase transferase protein serine/threonine-
protein ATP-binding II phosphorylation casein alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     osteoporosis, disorders of the immune system, e.g. inflammatory, diabetes mellitus, osteoarthritis and asthma. Proteins of the invention any also be of use as therapeutic agents in cardiovascular disorders such as hypertension and coronary artery disease, and some endothelial cell disorders, including psoriasis. The current sequence represents a human kinase 14257 amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New 14257 polypeptides (protein kinases), useful as diagnostic target and therapeutic agents for controlling cellular proliferative and/or differentiative disorder, bone disorders, immune disorders and
                                                                                                                                                                                                                                                 /note= "serine/threonine protein kinase active-site
signal site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "casein kinase II phosphorylation site"
                                                                                                                                                                          "casein kinase II phosphorylation site
                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "casein kinase II phosphorylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "tyrosine kinase phosphorylation site"
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18
                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABI16176-ABI30511), expressed DNA sequences (ABI01840-ABI16175) and the encoded proteins (ABB57377-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61.8%; Score 1027.5; DB 4; Length 392;
                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 16146; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Sequence 228 AA;

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PNLVNLIEVFRKKRKRKHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                                                                        121 NCIHRDIKPENILITKQGIIKICDFGFAQILIFGDAYTDYVATRWYRAPELLVGDTQYGS 180
                                                                                                                                                      SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGISIP 240
                                                                                                                                                                                                       181 PVDVWAIGCLFAELVRGEALWPGRSDVDQLYLIRKTLGDLLPRHIQIFGQNEYFKGITLP 240
                                                                                                                                                                                                                                          EPEDMETLEEKF---SDVHPVALNFWKGCLKMNPDDRLTCSQLLESSYFDSF--QEAQIK 295
                                                                                                                                                                                                                                                          241 VPPTLEPLEDKMPAKSQQNPLTIDFLKKKCLDKDPTKRWSCEKLTKHSYFDDYIAKQRELE 300
                                           9
                                                                  9
                                                    MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                   Gaps
                  2;
                 Indels
     pred. No. 1.5e-100;
65; Mismatches 61;
   Pred. No.
                                                                                                                                                                                                                                                                                           RKARNEGRNRRROOV 310
                                                                                                                                                                                                                                                                                                           | | |:||:
HVNSLEAANLROQOL 315
 58.4%;
             Matches 184; Conservative
Best Local Similarity
                                                                                       61
                                                                                                                                                                121
                                                                                                               61
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AAY90724 standard; protein; 566 AA. AAY90724; RESULT 15 AAY90724

(first entry) 15-AUG-2000

Rabbit KKIAMRE kinase SEQ ID NO:4.

Rabbit; KKIAMRE kinase; learning-induced kinase; learning; memory; cdc2-related kinase; brain; gene therapy; genetic disorder; detection; identification.

Oryctolagus cuniculus.

WO200020567-A2.

13-APR-2000

99WO-US023010 01-OCT-1999;

98US-0102906P 02-OCT-1998; (UYSC-) UNIV SOUTHERN CALIFORNIA.

Sun W; Gomi H, Thompson RF,

WPI; 2000-328932/28. N-PSDB; AAA29745

The present sequence represents a learning-induced kinase, designated KKIAMRE kinase, which is isolated from rabbit brain tissue. KKIAMRE kinase is a cdc2-related kinase. The KKIAMRE kinase polymodieotides can be used to express recombinant protein for analysis, characterisation or therapeutic use, as markers for tissues in which the protein is preferentially expressed, as molecular weight markers on Southern gels, as chromosome markers or tags, to compare endogenous DNA sequences in patients to identify potential genetic disorders, as probes to hybridise and discover novel related sequences, as a source of PCR primers, and as Novel learning induced kinase polynucleotides and polypeptides, useful for the analysis of learning and memory, and for gene therapy. Claim 1; Fig 4; 64pp; English.

ŭ PNLVNLIEVFRRKRKRMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120 120 239 240 9 assay to discover biological activity, to raise antibodies, as tissue markers, and to isolate correlative receptors or ligands. The polymucleotides may also be used for gene therapy for the treatment of disorders which are mediated by KKIAMKE kinase 1 MEKYENLGLVGEGSYGMVMKCRNKDSGRIVALKKFLESDDDKMVKKTAMREIKLLKQLRH 121 NCIHRDIKPENILITKQGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGDTQYG 180 SSVDIWAIGCVFAELLIGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGISI PEPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRLTCSQLLESSYF--DSF-----QEA 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH Gaps 15; Length 566; Indels 65; DB 3; 58.2%; Score 967.5; DB 3 54.6%; Pred. No. 6.9e-94; ive 67; Mismatches 65. 293 QIK--RKARN-----EGRNRRRQO 309 301 OMKVOKDARNISLSKKSONRKKEK 324 Query Match
Best Local Similarity 54.6
Matches 177; Conservative Sequence 566 AA; 240 8888888 ⋩ g ò g 셤 ò 셤 Š g ò ò

completed: April 22, 2005, 06:47:32 He : 88.5529 secs Search

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April 22, 2005, 04:37:19 ; Search time 30.929 Seconds (without alignments) 760.272 Million cell updates/sec
                                                                                                                                                                                                                                                                 1 MEKYEKLAKTGEGSYGVVFK.....RKARNEGRNRRRQQVLPLKS 315
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                               513545 segs, 74649064 residues
                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Run on:

513545 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CTIMMADITE

		•			SUMMARIES		
Result No.	Score	Query Match	Length	DB	ID	Description	
-	1662	100.0	315	4	US-09-671-050-12	Sequence 12, Appl	
8	1638	98.6	324	4	US-09-671-050-6	. 9	
٣	1636	98.4	347	4	US-09-671-050-10	Sequence 10, Appl	
4	1612	97.0	356	4	US-09-671-050-4	4	
'n	1188.5	71.5	367	4	US-09-949-016-7552	75	
9	1183.5	71.2	358	4	US-09-411-628-11	_	
7	1183.5	71.2	. 358	4	US-10-174-794-11	11,	
œ	967.5	58.2	266	4	US-09-411-628-4	4,	
σ	967.5	58.2	266	4	US-10-174-794-4	4	
10	941.5	56.6	475	4	US-09-949-016-7954	79	
11	941.5	56.6	493	4	US-09-411-628-10		
12	941.5	56.6	493	4	US-10-174-794-10	10,	
13	791	47.6	187	4	US-09-671-050-2	2,	
14	791	47.6	198	4	US-09-671-050-8	8	
15	581	35.0	305	4	US-09-538-092-1236	123	
16	581	35.0	305	4	US-09-949-016-6052		
17	581	35.0	334	4	US-09-949-016-10777	107	
18	570	34.3	298	~	US-08-874-347-25	25,	
19	570	34.3	298	7	US-08-969-106-2	2, 1	
20	570	34.3	298	m	US-09-093-522-25	25	
21	570	34.3	298	4	US-09-338-125-2	7	
22	570	34.3	298	4	09-266-2	14, 7	
23	570	34.3	544	4	US-09-417-197-113	113,	
24	570	34.3	544	4	US-09-417-197-115	Sequence 115, App	
25	569	34.2	298	4	US-09-411-628-13	13, #	
56	569	34.2	298	4	US-10-174-794-13	13,	
27	568.5	34.2	294	N	US-08-874-347-26	26.	

Sequence 26, Appl	Sequence 29, Appl	Sequence 1006, Ap	Sequence 8025, Ap	Sequence 16, Appl	Sequence 16, Appl	Sequence 23, Appl	Sequence 23, Appl	Sequence 24, Appl	Sequence 24, Appl	Sequence 12, Appl	Sequence 12, Appl	Sequence 10, Appl	Sequence 10, Appl	Sequence 31, Appl	Seguence 20, Appl	Sequence 20, Appl	1067
US-09-093-522-26	US-09-457-040B-29	US-09-538-092-1006	US-09-949-016-8025	US-08-176-620A-16	US-08-461-985-16	US-08-874-347-23	US-09-093-522-23	US-08-874-347-24	US-09-093-522-24	US-09-411-628-12	US-10-174-794-12	US-08-874-347-10	US-09-093-522-10	US-07-857-224B-31	US-08-318-947A-20	US-08-795-303-20	US-09-949-016-10673
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294	298	298	354	297	297	297	297	297	297	297	297	300	300	270	274	274	299
34.2	34.1	34.1	34.1	34.0	34.0	33.5	33.5	33.5	33.5	33.5	33.5	33.4	33.4	33.4	33.2	33.2	. 33.2
568.5	567	267	267	265	265	557	557	556	556	556	556	555.5	555.5	555	551	551	551
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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6.1 PNLVNLIEVFRRKRRYGMILVFEYCDHTLLNELERNPNGVADGVIKSVLMQTLQALNFCHIH 120
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                                                                                      APPLICANT: DOMONO, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Tradarich, Glenn
APPLICANT: Sanbrowicz, Brian
APPLICANT: Zanbrowicz, Brian
APPLICANT: Zands, Arthur T.
TITE OF INVENTION: Polynucleotides Encoding the Same
TITE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0046-USA
CURRENT APPLICATION NUMBER: US/09/671,050
CURRENT APPLICATION NUMBER: US 60/156,511
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PASESEQ for Windows Version 4.0
IENGTH: 315
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100.0%; Score 1662; DB 4; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.1e-166;
Matches 315; Conservative 0; Mismatches 0; Indels 0
                  Sequence 12, Application US/09671050 Patent No. 6716616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: homo sapiens
                                                                      GENERAL INFORMATION:
JS-09-671-050-12
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Gaps

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181 SVDIWAIGCVFAELLIGOPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGISIP 240

SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGISIP 240

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0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
FILE REFERENCE: LEX-0046-USA
CURRENT APPLICATION NUMBER: US/09/671,050
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: US 60/156,511
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09671050 Patent No. 6716616 GENERAL INFORMATION:
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Best Local Similarity 90.6%;
Matches 310; Conservative
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 90.8
Matches 315; Conservative
                                                                                                                                                                                                                          TYPE: PRT
CRGANISM: homo sapiens
US-09-671-050-10
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APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Newlis, Michael
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambs, Arrhur T.
TITLE OF INVENTION: Polymucleotides Encoding the Same
TITLE OF INVENTION: Polymucleotides Encoding the Same
TITLE OF INVENTION: Polymucleotides Encoding the Same
TITLE OF INVENTION: WOMBER: US/09/671,050
CURRENT FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 324
TYPE: PRT
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98.6%; Score 1638; DB 4; Length 324;
Best Local Similarity 100.0%; Pred. No. 3.8e-164;
Matches 310; Conservative 0; Mismatches 0; Indels
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APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nehls, Michael
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Of 7166161 Human Kinase Proteins and
TITLE OF INVENTION: Polynucleotides Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-671-050-10; Sequence 10, Application US/09671050; Patent No. 6716616; GENERAL INFORMATION:
                                                                                                                                                   5.09-671-050-6
Sequence 6, Application US/09671050
Patent No. 6716616
          301 EGRNRRRQQVLPLKS 315
                                                     EGRNRRRQOVLPLKS 315
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US-09-671-050-6
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                                                                                                                                               1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
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                                                                         32;
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APPLICANT: Turner, C. Alexander. Jr.
APPLICANT: Huner, C. Alexander. Jr.
APPLICANT: Striction, Glenn
APPLICANT: Zembrowicz, Brian
APPLICANT: Sambrowicz, Brian
APPLICANT: Sambrowicz, Brian
APPLICANT: Sambrowicz, Brian
APPLICANT: Sambrowicz, Brian
APPLICANT: Sambrowicz, Brian
APPLICANT: PINUETTION: No. 6716616el Human Kinase Proteins and
TITLE OF INVENTION: Polymucleotides Encoding the Same
FILE REPERENCE: LEX-0046-USA
CURRENT APPLICATION NUMBER: US/09/671,050
CURRENT FILING DATE: 2001-06-11
PRIOR FILING DATE: 1999-09-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 MNPDDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQQVLPLKS 347
   Length 347;
                                                                     Indels
Score 1636; DB 4;
Pred. No. 6.9e-164;
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Pred. No. 2.4e-161;
0; Mismatches 0;
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61 PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
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Patent No. 6664086

GENERAL INPORMATION:
TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
TITLE OF INVENTION: EDGURNCES OF LEARNING-INDUCED KINASES
TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
FILE REFERENCE: 13761-707
CURRENT FILING DATE: 2002-06-18
PRIOR PAPLICATION NUMBER: US/10/174,794
PRIOR APPLICATION NUMBER: US/09/411,628
PRIOR PILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: US 60/102,906

PRIOR PLING DATE: 1999-10-01

PRIOR PLING DATE: 1999-10-01

PRIOR SEQ ID NOS: 16

NUMBER OF SEQ ID NOS: 16
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                                                                                                                                                                                                                                                            TITLE OF INVERTION : CDNA, GENOMIC, AND PREDICTED PROTEIN TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES CURRENT APPLICATION NUMBER: US/09/411,628 CURRENT FILING DATE: 1999-10-01 EARLIER APPLICATION NUMBER: US 60/102,906 EARLIER APPLICATION NUMBER: US 60/102,906 EARLIER FILING DATE: 1998-10-02 NUMBER OF SEQ ID NOS: 16 SOFTWARE: FRASESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.2%; Score 1183.5; DB 4; 71.8%; Pred. No. 3.6e-116; Live 41; Mismatches 41;
                                                                                                                                                                                     Sequence 11, Application US/09411628
Patent No. 6428994
GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Homo sapiens
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US-10-174-794-11
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                                      |:
311 NK 312
        300 NE 301
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LENGIH: 358
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Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FESTESEQ for Windows Version 4.0

SEQ ID NO 7552
                                                                                                            61 PNLVNLIEVFRRKRKWHLVFEYCOHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 MNPDDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQQV 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 MNPDDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQQV 342
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US-09-949-016-7552
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Sequence 4, Application US/10174794

Patent No. 6664086

GENERAL INFORMATION:
TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
FILE REPERBANCE: 13761-707
CURRENT PELLING DATE: 13761-707

CURRENT FILING DATE: 1999-10-01
PRIOR PILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
SPRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
SPRIOR FILING DATE: 1999-10-01
SPRIOR FILING DATE: 1999-10-02
SOFTWARE: FASESEQ FOR WINDOWS VERSION 4.0
301 QMKVQKDARNISLSKKSQNRKKEK 324
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LENGTH: 566
                                                                               US-10-174-794-4
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                   DB 4; Length 358;
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GENERAL INFORMATION:

TITLE OF INVENTION: EDNA, GENOMIC, AND PREDICTED PROTEIN

TITLE OF INVENTION: EDNA, GENOMIC, AND PREDICTED PROTEIN

TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES

FILE REFERENCE: 13761-707

CURRENT APPLICATION NUMBER: US/09/411,628

CURRENT APPLICATION NUMBER: US 60/102,906

EARLIER FILING DATE: 1999-10-02

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 566
                                                         41; Indels
               71.2%; Score 1183.5; DB 4; 71.8%; Pred. No. 3.6e-116; iive 41; Mismatches 41;
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Patent No. 6428994
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; ORGANISM: Orcytolagus cuniculus
US-09-411-628-4
            Query Match
Best Local Similarity 71.8*
Matches 211; Conservative
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; Sequence 7954, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,756
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-00-03
; PRIOR FILING DATE: 2000-00-09
; PRIOR FILING DATE: 2000-00-09
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                                                                                                                                               Gaps
                                                                                                                                            15;
                                                                                      DB 4; Length 566;
                                                                                                                                            Indels
                                                                                                                                            65;
                                                                                Query Match 58.2%; Score 967.5; DB 4 Best Local Similarity 54.6%; Pred. No. 4.2e-93; Matches 177; Conservative 67; Mismatches 65
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ORGANISM: Orcytolagus cuniculus
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US-10-174-794-10
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                                                                                                                         56.6%; Score 941.5; DB 4; Length 475; 53.1%; Pred. No. 1.8e-90; ive 68; Mismatches 69; Indels 15
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TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
FILE REFERENCE: 13761-707
CURRENT APPLICATION NUMBER: US/09/411,628
CURRENT FILING DATE: 1999-10-01
EARLIER APPLICATION NUMBER: US 60/102,906
EARLIER FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 16
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 56.6%; Score 941.5; DB 4 Best Local Similarity 53.1%; Pred. No. 1.9e-90; Matches 172; Conservative 68; Mismatches 69
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 7954
LENGTH: 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 QIK--RKARN-----EGRNRRRQQ 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:| : ||| : ||303 QLKVQKDARNVSLSKKSQNRKKEK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/09411628
                                                                                                                         Query Match
Best Local Similarity 53.1<sup>3</sup>
Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-411-628-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6428994
GENERAL INFORMATION:
                                                   ; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-411-628-10
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61 PNLVNLIEVFRRKRKMHLVFBYCDHTLINELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCIHRDIKPENILITKQGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGDTQYG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 SSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGISI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRLTCSQLLESSYF--DSF----QEA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MEKYENLGLVGEGSYGWVMKCRNKDTGRIVAIKKFLESDDDKMVKKIAMREIKLLKQLRH 60
                                                                                                  PEPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRLTCSQLLESSYF--DSF----QEA
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                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/10174794

Patent No. 6664086

GENERAL INPORMATION:
TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
TITLE REFERENCE: 13761-707

CURRENT APPLICATION NUMBER: US/10/174,794

CURRENT FILING DATE: 2002-06-18

PRIOR FILING DATE: 1999-10-01

PRIOR FILING DATE: 1999-10-01

PRIOR FILING DATE: 1999-10-01

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.6%; Score 941.5; DB 4
53.1%; Pred. No. 1.9e-90;
tive 68; Mismatches 69
                                                                                                                                                                                                                              |:| : ||| : ||301 QLKVQKDARNVSLSKKSQNRKKEK 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 QIK--RKARN-----EGRNRRRQQ 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 53.13
Matches 172; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Newles, Michael
APPLICANT: Friedrich, Glenn
APPLICANT: Sambrowicz, Brian
APPLICANT: Sambrowicz, Brian
APPLICANT: Sambrowicz, Brian
APPLICANT: Sambrowicz, Brian
APPLICANT: Sambrowicz, Brian
APPLICANT: Sambrowicz, Brian
APPLICANT: Sambrowicz, Brian
APPLICANT: Sambrowicz, Brian
APPLICANTON: NO: 6716616el Human Kinase Proteins and
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0046-USA
CURRENT FILING DATE: 2001-06-11
PRIOR PAPLICATION NUMBER: US 60/156,511
PRIOR PELING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE FREUER: RESURE FOR Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match

47.6%; Score 791; DB 4; Length 187;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
Matches 151; Conservative 0; Mismatches 0; Indels
               APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
TITLE OF INVENTION: POLYNUCLECTIONS Encoding the Same
FILE REFERENCE: LEX-0046-USA
CURRENT APPLICATION NUMBER: US/09/671,050
PRIOR APPLICATION NUMBER: US 60/156,511
PRIOR PILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
47.6%; Score 791; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 3.6e-75;
Matches 151; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 NCIHRDIKPENILITKOGIIKICDFGFAQIL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/09671050
Patent No. 6716616
Friedrich, Glenn
                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CAGANISM: homo sapiens
US-09-671-050-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: homo sapiens
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LENGTH: 198
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Sequence 1236, Application US/09538092
| Beten No. 675334
| GENERAL INFORMATION:
| APPLICANT: Giot, Loic
| APPLICANT: Giot, Loic
| APPLICANT: Mansfield, Traci A.
| TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REFERENCE: 15966-542
| CURRENT FILING DATE: 2000-03-29
| PRIOR PAPLICATION NUMBER: 60/127,352
| PRIOR FILING DATE: 2000-03-29
| PRIOR FILING DATE: 1999-04-01
| PRIOR FILING DATE: 2000-03-05
| WINDER OF SEQ ID NOS: 1387
| SOFTWARE: CURAPACSGFORMATHER VERSION 0.9
| SEQ ID NO 1236
| LENGTH: 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 GVTQLPDYKGSFPKWTRKGLEEIVPNLEPEGRDLLMQLLQYDPSQRITAKTALAHPYFSS 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
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1662
1 MEKYEKLAKTGEGSYGVVFK......RKARNEGRNRRRQQVLPLKS 315
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

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                                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Appl	Appl	1pp]i	Appl	\ppli	Apr	Appl	Appl	pli	\pp1i	Appl	Appl	App
_	12,	10,	6, 1	10,	4, 7	391,	97,	11,	, Ag	4, 7	10,	22,	108,
Description	Sequence 12, App	Sequence	Sequence	Sequence 10, Appl	Sequence	Sequence	Sequence	Sequence	Sequence 2	Sequence	Sequence	Sequence	Sequence
ΙD	US-10-766-691-12	US-10-333-314-10	US-10-766-691-6	US-10-766-691-10	US-10-766-691-4	US-10-363-616-391	US-10-664-421-97	US-10-174-794-11	US-09-834-496A-2	US-10-174-794-4	US-10-174-794-10	US-10-369-022-22	US-10-757-262-108
	17	15	17.	17	17	15	16	14	6	14	14	15	16
* Query Match Length DB	315	342	324	347	356	358	338	358	228	995	493	493	493
% Query Match	100.0	98.6	98.6	98.4	97.0	71.5	71.4	71.2	68.6	58.2	56.6	9.95	56.6
Score	1662	1639	1638	1636	1612	1188.5	1186.5	1183.5	1140	967.5	941.5	941.5	941.5
Result No.		7	m	4	S	9	7	80	σ	10	11	12	13

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Gaps

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Query Match
Best Local Similarity 100.0%; Pred. No. 2e-132;
Matches 315; Conservative 0; Mismatches 0; Indels 0;

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Sequence 2, Appli Sequence 34, Appli Sequence 62, Appl Sequence 64, Appl Sequence 14, Appl Sequence 113, Appl Sequence 113, Appl Sequence 113, Appl Sequence 113, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 18, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 133, Appl Sequence 133, Appl Sequence 133, Appl Sequence 134, Appl Sequence 137, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 12, Appl Sequence 12, Appl	
US-10-766-691-2 US-10-766-691-8 US-10-250-689-62 US-10-250-889-62 US-10-394-322A-8 US-10-620-628-220 US-10-620-628-220 US-10-620-628-113 US-10-77-1613-187 US-10-77-036-115 US-10-72-036-113 US-10-73-681-27 US-10-295-681-27 US-10-620-628-55 US-10-644-21-14 US-10-644-421-14 US-10-295-681-31 US-10-295-681-31 US-10-295-681-31 US-10-295-681-32 US-10-295-681-33 US-10-295-681-33 US-10-295-681-33 US-10-295-681-33 US-10-295-681-33 US-10-295-681-32 US-10-295-681-32 US-10-295-681-33 US-10-295-681-33 US-10-295-681-35 US-10-295-681-35 US-10-295-681-35 US-10-295-681-35 US-10-295-681-35 US-10-295-681-35 US-10-295-681-35 US-10-295-681-35 US-10-295-681-35 US-10-295-681-35 US-10-295-681-35 US-10-295-681-35 US-10-295-681-35 US-10-295-681-35 US-10-395-681-35 US-10-395-681-35 US-10-395-681-35 US-10-395-681-35 US-10-395-681-35 US-10-395-681-35 US-10-395-681-35 US-10-395-681-35 US-10-395-681-35 US-10-395-681-35	on US/10766691 10042626A1 10042626A1 10. Alexander Jr. 10. Alexander Jr. 10. Glean 12. Brian 12. Brian 12. Brian 12. Glean 13. Brian 14. Glean 15. Glean 16. Glean 17. Glean 18. Same 18. US/10/766,691 2004-01-28 18. US/10/766,691 2004-01-28 18. US/09/671,050 19.0-09-27 13. Windows Version 4.0
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4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	ULT 1 10-766-691-12 equence 12, Application US/1 ublication No. US20050042626, ENERAL INFORMATION: RAPLICANT: Donoho, Gregory APPLICANT: Nehls, Michael APPLICANT: Sambrowicz, Bria APPLICANT: Sambrowicz, Bria APPLICANT: Sambrowicz, Bria APPLICANT: Sands, Arthur T. ITTLE OF INVENTION: Novel Hun ITTLE OF INVENTION: Polynuc FILE REFERENCE: LEX-0046-USA CURRENT APPLICATION NUMBER: US PRIOR PLIING DATE: 2000-09-2 PRIOR FILING DATE: 1999-09-2 NUMBER OF SEQ ID NOS: 13 SOGTWARE: FASISEQ for WINGOR ELENGTH: 315 LENGTH: BRT
791 791 791 791 791 701 581 580 567 567 567 567 567 567 567 567 567 567	SULT 1 10-766-691-12 Sequence 12, Applic Sequence 12, Applic GENERAL INFORMATION APPLICANT: Donoho, APPLICANT: Turner APPLICANT: Turner APPLICANT: Turner APPLICANT: Sambro APPLICANT: Sambro APPLICANT: Sambro APPLICANT: Sambro APPLICANT: Sambro APPLICANT: Bender, TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION THEN APPLICATION OURRENT APPLICATION SPRIOR FILING DATE: NUMBER OF SEQ ID N SOFTWARE: FASTESC TYPE: PRT ORGANISM: homo sa -10-766-691-12
1 1 1 1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2	RESULT 1 US-10-766-69; Sequence 1; Sequence 1; Publication; APPLICANT TITLE OF TITLE

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61 PNLVNLIEVFRRKRYMHLVFEYCDHTLINELERNPNGVADGVIKSVLWQTLQALNFCHTH 120
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                                                                           PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH
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APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: The Methal
APPLICANT: Tedrich, Glenn
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
CURRENT: Sands, Arthur T.
APPLICANTON: Polynucleotides Encoding the Same
TITLE OF INVENTION: Polynucleotides Encoding the Same
TITLE OF INVENTION: Polynucleotides Encoding the Same
TITLE APPLICATION NUMBER: US/09/671,050
FRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/156,511
PRIOR APPLICATION NUMBER: US 60/156,511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           эчь*; Score 1638; DB 17;
100.0%; Pred. No. 2.2e-130;
ive 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/1076691; Publication No. US20050042626A1; GENERAL INFORMATION:
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EGRNRRRQQNQLLPL 315
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Best Local Similarity 100.
Matches 310; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: homo sapiens
US-10-766-691-6
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                                                       61 PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH
                                                                                                                                                 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKTALREIRMLKQLKH
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APPLICANT: HARALIA, PARTA A: GURURALAN, Rajagopal
APPLICANT: HARALIA, April J.A.; CHAWLA, Narinder K.
APPLICANT: HARALIA, April J.A.; CHAWLA, Narinder K.
APPLICANT: GANDHI, Chandra S.; RAWKUMAR, Jayabaxmi
APPLICANT: GANDHI, Ameena R.; POLICKY, Jennifer L.
APPLICANT: GAUGHN, Mariah R.; TRIBOULEY, Catherine M.
APPLICANT: HOUVEN, Danniel B.; LU, Yan
APPLICANT: HURFORD, Neil; LAL, Preeti G.
APPLICANT: BURFORD, Neil; LAL, Preeti G.
APPLICANT: BURFORD, Neil; LAL, Preeti G.
APPLICANT: BURFORD, Neil; LAL, Preeti G.
APPLICANT: GEREWALD, Sara R.; TRNG, T. TOM
APPLICANT: GREEWALD, Sara R.; TRNG, T. TOM
APPLICANT: GIETEN, Kimberly J.; YANG, Junming
APPLICANT: GIETEN, Kimberly J.; YANG, Junming
APPLICANT: JACKSON, Jennifer L.
TITLE OF INVENTION: HUPAN KINASES
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/220,038
PRIOR PELING DATE: 2000-07-21
PRIOR PELING DATE: 2000-07-21
PRIOR PELING DATE: 2000-07-21
PRIOR PELING DATE: 2000-07-21
PRIOR PELING DATE: 2000-07-21
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OTHER INFORMATION: Incyte ID No: 1698381CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/10333314
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Publication No.
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61 PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWOTLQALNFCHIH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCIHRDIKPENILITKQGIIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTQYGS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 NCIHRDIKPENILITKQGIIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTQYGS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 97.0%; Score 1612; DB 17; Length 356; Best Local Similarity 90.6%; Pred. No. 3.9e-128; Matches 310; Conservative 0; Mismatches 0; Indels 32.
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Publication No. US20040044181A1
GENERAL INPORMATION:
APPLICANT: Hyeeq. Inc
FILE REFERENCE: 21272-113 (793)
CURRENT APPLICATION NUMBER: US/10/363,616
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 09/654,935
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 490
                     APPLICANT: Sands, Arthur T.

TITLE OF INVENTION: Novel Human. Kinase Proteins and
TITLE OF INVENTION: Polynucleotides Encoding the Same
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0046-USA
CURRENT APPLICATION NUMBER: US/07/66,691
CURRENT FILING DATE: 2004-01-28
PRIOR APPLICATION NUMBER: US 60/156,511
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 4
LENGTH: 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 MNPDDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQQV 342
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                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: homo sapiens
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-391
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241 EPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRLTCSQLLESSYFDSFQEAQIKRKARN 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 PNLVNLIEVFRRKRKRMHLVFEYCDHTLLNBLERNPNGVADGVIKSVLWQTLQALNFCHIH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.4%; Score 1636; DB 17; Length 347; 90.8%; Pred. No. 3.5e-130; tive 0; Mismatches 0; Indels 32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 MNPDDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQQVLPLKS 315
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APPLICANT: Doublo, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nehls, Michael
APPLICANT: Triedrich, Glenn
APPLICANT: Sands, Arthur T.
TILE OF INVENITON: Polynucleotides Encoding the Same
TILE REPERENCE: LEX-0046-USA
TILE REPERENCE: LEX-0046-01-28
FRICH PAPLICATION NUMBER: US/09/671,050
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nehls, Michael
APPLICANT: Friedrich, Glenn
                                                                                                                                                                                                                          Sequence 10, Application US/10766691
Publication No. US20050042626A1
GENERAL INFORMATION:
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Publication No. US20050042626A1
GENERAL INFORMATION:
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301 EGRNRRRQQV 310
                                                   301 EGRNRRRQQV 310
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Best Local Similarity
Matches 315; Conserv
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US-10-766-691-4
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121 NCIHRDIKPENILITKQGIIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTQYG 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
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Fatent No. US20020000701A1
GENERAL INFORMATION:
TITLE OF INVENTION: 14257 NOVEL PROTEIN KINASE MOLECULES AND TITLE OF INVENTION: THEIR USES THEREFOR
FILE REPERRENCE: 38152000900
CURRENT APPLICATION NUMBER: US/09/834,496A
CURRENT PILING DATE: 2000-04-13
FRIOR APPLICATION NUMBER: 60/196,910
FRIOR FILING DATE: 2000-04-13
FRIOR FILING DATE: 2000-04-13
FRIOR FILING DATE: 2000-04-13
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FRIOR FILING DATE: 2000-04-13
FRIOR FILING DATE: 2000-04-13
FRIOR FILING DATE: 2000-04-13
                                                                                                                                                             sequence 11, Application US/10174794

| Publication No. US20030166220A1
| Publication No. US20030166220A1
| Publication No. US20030166220A1
| TELE CARLOWENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
| TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
| FILE REFERENCE: 13761-707
| CURRENT APPLICATION NUMBER: US/10/174,794
| PRIOR PLING DATE: 1999-10-01
| PRIOR FILING DATE: 1999-10-02
| NUMBER OF SEQ ID NOS: 16
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
US-10-174-794-11
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ORGANISM: Homo sapiens
                     300 NE 301
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302 NK 303
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                                           PNLVNLIEVFRRKRKRMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                 62 PNLVNLLEVFRRKRRLHLVFEYCDHTVLHELDRYQRGVPEHLVKSITWQTLQAVNFCHKH 121
                                                                                                                            NCIHRDIKPENILITKOGIIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTQYG 179
                                                                                                                                                    180 SSVDIWAIGCVFAELLIGQPLMPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGISI 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 97, Application US/10664421
| Sequence 97, Application US/10664421
| Publication No. US20040142864A1
| GENERAL INPORMATION:
| APPLICANT: BREMER, RYAN
| APPLICANT: BRAHIM, RRABHA
| APPLICANT: MANDIYAN, VALSAN
| APPLICANT: MANDIYAN, VALSAN
| APPLICANT: MANDIYAN, VALSAN
| APPLICANT: MANDIYAN, VALSAN
| APPLICANT: MILBURN, MICHAEL V
| TITLE OF INVERTION: COSTON OF 16 CONTRENT FILING DATE: 2003-09-16
| PRIOR FILING DATE: 2003-09-16
| PRIOR PRILING DATE: 2002-09-16
| PRIOR FILING DATE: 2002-09-16
| NUMBER OF SEQ ID NOS: 169
| SOFTWARE PATENTIN VOT: 3.2
| SEQ ID NO 97
| TENGRIE: PATENTIN VOT: 3.2
| SEQ ID NO 97
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Best Local Similarity 70.5$
Matches 213; Conservative
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US-10-664-421-97
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NK 303
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                                                                                                                                      PNLVNLIEVPRRKKKRMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
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                                                                                         1 MEKYENLGLVGEGSYGWYMKCRNKDSGRIVAIKKFLESDDDKMYKKIAMREIKLLKQLRH
                                                                      1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
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                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/10174794

Sequence 4, Application US/10174794

Publication No. US20030166220A1

GENERAL INPORMATION:

APPLICANT: University of Southern California

TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN

TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES

TITLE REFERENCE: 1376-1707

CURRENT FILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: US/09/411,628

PRIOR APPLICATION NUMBER: US 60/102,906

PRIOR FILING DATE: 1999-10-01

PRIOR FILING DATE: 1999-10-01

PRIOR PLING DATE: 1999-10-01

SOFTWARE: FastSEQ for Windows Version 4.0
     DB 9; Length 228;
                                      Indels
                                                                                                                                                                                                                                                                          SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLG 218
                                                                                                                                                                                                                                                                                                           181 SVDIWAIGCVFAELLTGOPLWPGKSDVDOLYLIIRTLG 218
 Score 1140; DB 9
Pred. No. 2e-88;
2; Mismatches
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     68.6%;
98.2%;
Query Match
Best Local Similarity 98.2'
Matches 214; Conservative
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LENGTH: 566
TYPE: PRT
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Sequence 22, Application US/10369022

Sequence 22, Application US/10369022

Publication No. US20030203847A1

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US-10-174-794-10

Sequence 10, Application US/10174794

Sequence 10, Application US/10174794

Publication No. US20030166220A1

GENERAL INFORMATION:

TITLE OF INVENTION: ENAL GENOMIC, AND PREDICTED PROTEIN

TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES

FILE REFERENCE: 13761-707

CURRENT APPLICATION NUMBER: US/09/411,628

PRIOR FILING DATE: 2002-06-18

PRIOR FILING DATE: 1999-10-01

PRIOR FILING DATE: 1999-10-02

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PRESERE FOR Windows Version 4.0

SEQ ID NO 10

LENGTH: 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 QIK--RKARN-----EGRNRRRQQ 309
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ORGANISM: Homo sapiens
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US-10-369-022-22
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REFERENCE: MPI03-007P1RNOMNIM
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APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18660, 2047,
TITLE OF INVENTION: 33751, 52872, 14663, 20739, 32844, 43239, 44373, 51164,
TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41837, 11TLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
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53.1%; Pred. No. 3.2e-71;
Live 68; Mismatches 69; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        See File Wrapper or PALM
PRIOR FILING DATE: 2002-04-04
PRIOR PELING DATE: 2002-04-16
PRIOR PELING DATE: 2002-04-16
PRIOR PELING DATE: 2002-04-19
PRIOR PLING DATE: 2002-04-19
PRIOR PLING DATE: 2002-04-19
PRIOR PLING DATE: 2002-05-03
PRIOR PLING DATE: 2002-05-03
PRIOR PLING DATE: 2002-05-13
PRIOR PLING DATE: 2002-05-13
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PRIOR PLING DATE: 2002-05-13
PRIOR PLING DATE: 2002-06-13
PRIOR PLING DATE: 2002-06-06
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Publication No. US20040197825A1
GENERAL INFORMATION:
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Best Local Similarity 53.1°
Matches 172; Conservative
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ORGANISM: Homo sapiens
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US-10-757-262-108
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61 PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
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APPLICANT: Donoho, Gregory
APPLICANT: Nehls, Michael
APPLICANT: Nehls, Michael
APPLICANT: Sambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Michael APPLICANT: TITLE OF INVENTION: Polynucleotides Encoding the Same
CURRENT APPLICATION NUMBER: US, 10/757, 262
CURRENT FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: US 60/440, 318
PRIOR APPLICATION NUMBER: US 60/440, 318
PRIOR PLILNG DATE: 2003-01-15
PRIOR PLILNG DATE: 2003-02-04
PRIOR PLILNG DATE: 2003-03-27
PRIOR PLILNG DATE: 2003-05-04
PRIOR PLILNG DATE: 2003-05-06
PRIOR PLILNG DATE: 2003-05-08
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PRIOR PLILNG DATE: 2003-07-07
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PRIOR PLILNG DATE: 2003-09-02
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Publication No. US20050042626A1
GENERAL INFORMATION:
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Best Local Similarity 53.1#
Matches 172, Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nehls, Michael
APPLICANT: Nehls, Michael
APPLICANT: Nehls, Michael
APPLICANT: Sambrowicz, Brian
APPLICANT: Sands, Arthur T.
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APPLICANT: Sonds, Arthur T.
APPLICANT: NOWBER: US, 10,766,691
CURRENT APPLICATION NUMBER: US, 10,766,691
FRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
SONTWARE: FRASESO for Windows Version 4.0
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47.6%; Score 791; DB 17;
Best Local Similarity 100.0%; Pred. No. 5.6e-59;
Matches 151; Conservative 0; Mismatches 0;
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                                                  CURRENT FILING DATE: 2004-01-28
PRIOR APPLICATION NUMBER: US/09/671,050
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/156,511
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
REFERENCE: LEX-0046-USA
ENT APPLICATION NUMBER: US/10/766,691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/1076691 Publication No. US20050042626A1 GENERAL INFORMATION:
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; LENGTH: 198
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-766-691-8
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CORGANISM: homo sapiens
US-10-766-691-2
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LENGTH: 187
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Search completed: April 22, 2005, 07:36:43 Job time: 781.363 secs

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8: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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PCT-USO5-03526-5
US-60-655-875-129900
PCT-USO5-03526-6
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      14313, A
114791, A
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118623, A
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US-10-941-635-71

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91.9%; Pred. No. 9.8e-89;
tive 6; Mismatches 14;
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Matches 294; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: BREMER, RYAN E.
APPLICANT: BLEMER, RYAN E.
APPLICANT: GILLETTE, SAMUEL J.
APPLICANT: GILLETTE, SAMUEL J.
APPLICANT: GILLETTE, SAMUEL J.
APPLICANT: GILLETTE, SAMUEL J.
APPLICANT: LIBRAHIM, PRABHA L.
APPLICANT: ZUCKERWAN, REBECCA L.
TITLE OF INVENTION: WOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
FILE REFERENCE: 039363-1702
CURRENT APPLICATION NUMBER: 05/04-09-15
FRIOR APPLICATION NUMBER: 06/503,277
RIOR FILING DATE: 2003-09-15
NUMBER OF SEQ ID NOS: 167
SEQ ID NO 97
LENGTH: 338
TYPE: PRT
ORGANISM: Unknown Organism
FRIOR FRIUND: CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT ON CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRACT OF CONTRAC
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                                                                                                                                   TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT FILE REFERENCE: 039363-1703
CURRENT APPLICATION UNBER: PCT/USO4/30360
CURRENT FILING DATE: 2004-09-15
PRIOR APPLICATION NUMBER: 60/503,277
PRIOR APPLICATION NUMBER: 60/503,277
NUMBER OF SEQ ID NOS: 167
SOFTWARE: Patentin Ver. 3.2
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                             Sequence 97, Application PC/TUS0430360 GENERAL INFORMATION:
APPLICANT: PLEXXIKON, INC.
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Best Local Similarity 71.8%
Matches 211; Conservative
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ORGANISM: Unknown Organism
PCT-US04-30360-97
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LENGTH: 338
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APPLICANT: EXELIXES, INC.

TITLE OF INVENTION: MEMS AS MODIFIERS OF BRANCHING MORPHOGENESIS AND METHODS OF USE
FILE REPERENCE: EXCS-003-CPC
CURRENT APPLICATION NUMBER: 9CT/USO5/03526
CURRENT FILING DATE: 2005-01-27
PRIOR PILING DATE: 2004-01-28
PRIOR FILING DATE: 2004-01-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.2
SEQ ID NO 5.
                                                                                                                         61 PNLVNLIEVFRKKKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
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      Length 338;
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                                   41; Indels
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    DB 6;
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53.1%; Pred. No. 6.4e-53;
tive 68; Mismatches 69;
    ; Score 1183.5; DB 6; Pred. No. 1.8e-68; 41; Mismatches 41;
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 71.2%;
Query Match
Best Local Similarity 71.8'
Matches 211; Conservative
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Best Local Similarity 53.1%
Matches 172; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: EXELIXIS, INC.

TITLE OF INVENTION: MBMS AS MODIFIERS OF BRANCHING MORPHOGENESIS AND METHODS OF USE.

FILE REPERENCE: EXGS-003-CPG
CURRENT APPLICATION NUMBER: PCT/USOS/03526

CURRENT FILING DATE: 2005-01-27

PRIOR APPLICATION NUMBER: USG0/539,835

PRIOR APPLICATION NUMBER: USG0/539,835

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin version 3.2

SEQ ID NO 8
                          USE
APPLICANT: EXELIXIS, INC.

TITLE OF INVENTITON: MBMS AS MODIFIERS OF BRANCHING MORPHOGENESIS AND METHODS OF UTILE REFERENCE: EXOS-003C-PC
CURRENT APPLICATION NUMBER: PCT/USOS/03526
CURRENT FILING DATE: 2005-01-27
PRIOR PILING DATE: 2005-01-28
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.2
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44.4%; Pred. No. 1.4e-38;
ative 69; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                       ; Score 784.5; DB 1;
; Pred. No. 5.8e-43;
61; Mismatches 91;
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 150; Conserv
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Matches 139; Conserv
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OTHER INFORMATION: Coding regions on vcDNA: vcDNA=SeqID 56323; Strand=+; Position=1
OTHER INFORMATION: -84,137-220,381-502,552-634,972-1052,1156-1312,1385-1452,1528
OTHER INFORMATION: -1615,2100-2218
FEATURE:
OTHER INFORMATION: Homolog annotation: Hit ID=XP_355031.2; Match level="QueryCoveragOTHER INFORMATION: =99%, HitCoverage=75%, E-value=8e-96, Identity=51%"; Hit descript OTHER INFORMATION: =similar to cyclin-dependent kinase-11ke 1 (CDC2-related kinase)
OTHER INFORMATION: musculus]
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                                                                                                                                                                                                                                                                                                                            APPLICANT: Wu, Wei
TITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
FILE PEPERENCE: 38-21 (53885)
CURRENT APPLICATION NUMBER: US/60/655,875
CURRENT FILING DATE: 2005-02-24
NUMBER OF SEQ ID NOS: 171306
SEQ ID NO 129900
LENGTH: 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIPEPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRLTCSQLLESSYFDS 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (324).. (324)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.7%; Score 909; DB 8; Length 350; 50.1%; Pred. No. 5.5e-51; ive 50; Mismatches 59; Indels
                                                                      Sequence 129900, Application US/60655875 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Heterodera glycines
                                                                                                                                                                                      Kovalic, Ďavid
Lu, Maolong
McCarter, James
Miller, Nancy
                                                                                                                                                                                                                                                                                   Williams, Deryck
Vaudin, Mark
                                                                                                                    APPLICANT: Boukharov, Andrey APPLICANT: Du, Zijing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.13
Matches 176; Conservative
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APPLICANT:
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61 PNLVNLIEVFRRKRKNAHLVFEYCDHTLINELERNP-NGVADGVIKSVLWOTLQALNFCHI 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PNIVKLEDVIHTENKLYLVFEFLHQDEKKFMDASALTGIPLFLIKSYLFQLLQGLAFCHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 HNCIHRDIKPENILITKQGIIKICDFGFAQIL-IPGDAYIDYVATRWYRAPELLVGDTQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 GSSVDIWAIGCVFAELLIGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGI-
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CURRENT APPLICATION NUMBER: PCT/USO4/30360
CURRENT FILING DATE: 2004-09-15
PRIOR PELLING DATE: 2003-09-15
NUMBER OF SEQ ID NOS: 167
SOFTWARE: Patentin Ver. 3.2
SOFTWARE: Patentin Ver. 3.2
LENGTH: 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 51, Application PC/TUS0430360
GENERAL INFORMATION:
DEPLICANT: PLEXXIVON, INC.

TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
FILE REPERENCE: 039363-1703
CURRENT APPLICATION NUMBER: PCT/US04/30360
CURRENT FILING DATE: 2004-09-15
PRIOR PLILING DATE: 2003-09-15
NUMBER OF SEQ ID NOS: 167
SOFTWARE: PATCHING DATE: 2003-09-15
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LENGTH: 298
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                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Description of Unknown Organism: Mammalian ; OTHER INFORMATION: protein sequence PCT-US04-30360-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Unknown Organism: Mammalian OTHER INFORMATION: protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.1%; Score 567; DB 1; Length 298;
40.0%; Pred. No. 2.8e-29;
Live 60; Mismatches 99; Indels
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Best Local Similarity 40.0%; Pred. No. 2.8e-29;
Matches 118; Conservative 60; Mismatches 99
                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Unknown Organism
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Best Local Similarity 40.08
Matches 118; Conservative
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LOCATION: (115)...(146)
OTHER INFORMATION: Protein kinases ATP-binding region proteins domain identified
OTHER INFORMATION: by eMATRIX, accession number BL00107A, p-value=8.500e-27, raw
OTHER INFORMATION: score of 18.39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (4)...(180)
OTHER INFORMATION: Bukaryotic protein kinase domain identified by PFam,
OTHER INFORMATION: accession name pkinase, E-value=3.5e-65, PFam score of 230.0
                                                                              70 ENIVELKEAFRRGKLYLVFEYVEKNMLELLEEMPNGVPPEKVKSYIYQLIKAIHWCHKN 129
                                                                                                                                                                          249 FPAVNHPQSLERRYLGILNSVLLDLAMKNLLKLDPADRYLTEQCLN---HPTFQTQRLLDR 305
                                                  NCIHRDIKPENILITKQGIIKICDFGFAQILIPGD--AYTDYVATRWYRAPELLVGDTQY 178
                                                                                                                                              179 GSSVDIWAIGCVFAELLIGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGIS 238
                                                                                                                                                                                                                                            239 IPEPEDMETLEEKFSDV-HPVALNFWKGCLKAMPDDRLTCSQLLESSYFDSFQEAQIKRK 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT PAPPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR PLING DATE: 2000-03-31
PRIOR PLING DATE: 2000-03-31
PRIOR PLING DATE: 2000-03-31
PRIOR PELING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
SPRIOR PILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SEQ ID NO 36501
LENGTH: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 36501, Application US/10450763; GENERAL INFORMATION:
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i Sequence 14, Application PC/TUS0430360
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: DOMAIN
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APPLICANT: GILLETTE, SANUEL J.
APPLICANT: HURT, CLARENCE R.
APPLICANT: HURT, CLARENCE R.
APPLICANT: HURT, CLARENCE R.
APPLICANT: SUCKEMAN, REBECCA L.
TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
FILE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
FILE REFERENCE: 039363-170
FILE OF INVENTION NUMBER: US/10/941,635
CURRENT APPLICATION NUMBER: 60/503,277
PRIOR FILING DATE: 2004-09-15
NUMBER OF SEQ ID NOS: 167
SOFTWARE: Patentin Ver: 3.2
SEQ ID NO 14
LENGTH: 298
TYPR: F.-
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                                                                                                                                                         120 HNCIHRDIKPENILITKQGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGDTQY 178
                                                                                                                                                                                                                                                                                                           179 GSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGI- 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 34.1%; Score 567; DB 6; Length 298; Best Local Similarity 40.0%; Pred. No. 2.8e-29; Matches 118; Conservative 60; Mismatches 99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-941-635-14
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HNCIHRDIKPENILITKQGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGDTQY 178
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APPLICANT: HAUPTS, Ulrich
APPLICANT: KOLTERMANN, Andreas
APPLICANT: SCHEIDIG, Andreas
APPLICANT: CHEIDIG, Andreas
APPLICANT: COCY
WAYNE MICHAEL
APPLICANT: COCO, WAYNE MICHAEL
TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
TITLE OF INVENTION: New Biological Entities And The Pharmaceutical
TITLE OF INVENTION: New Biological
FILE REFERENCE: 04156.0002U5
CURRENT APPLICATION NUMBER: US/11/021,951
CURRENT FILING DATE: 2004-06-18
PRIOR PELICATION NUMBER: 60/524,960
PRIOR PELING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: EP 04003058
PRIOR APPLICATION NUMBER: EP 04003058
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: EP 04003058
PRIOR FILING DATE: 2004-02-11
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APPLICANT: BREMEN, SAMUEL J.
APPLICANT: GILLETTE, SAMUEL J.
APPLICANT: GILLETTE, SAMUEL J.
APPLICANT: HURT, CLARENCE R.
APPLICANT: IBRAHIM; PRABHA L.
APPLICANT: ZUCKERMAN, REBECCA L.
TITLE OF INVENTION: MOLECULAR SCAPPOLDS FOR KINASE LIGAND DEVELOPMENT
FILE REPERENCE: 039363-1702
CURRENT APPLICATION NUMBER: US/10/941,635
PRIOR FILING DATE: 2004-09-15
PRIOR FILING DATE: 2003-09-15
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OTHER INFORMATION: Description of Unknown Organism: Mammalian
OTHER INFORMATION: protein sequence
US-10-941-635-51
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34.1%; Score 567; DB 6; Length 298;
Best Local Similarity 40.0%; Pred. No. 2.8e-29;
Matches 118; Conservative 60; Mismatches 99; Indels
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SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 51
LENGTH: 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Unknown Organism
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                                                                                                                                                                                             34.1%; Score 567; DB 7; Length 298; 40.0%; Pred. No. 2.8e-29; Live 60; Mismatches 99; Indels
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GENERAL INFORMATION:
APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21 (53629) A
CURRENT APPLICATION NUMBER: US/60/643,717
CURRENT FILING DATE: 2005-01-12
NUMBER OF SEQ ID NOS: 19247
LENGTH: 294
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33.8%; Score 561.5; DB 8;
Best Local Similarity 37.0%; Pred. No. 6.2e-29;
Matches 115; Conservative 69; Mismatches 92;
PRIOR FILING DATE: 2003-11-11
PRIOR APPLICATION NUMBER: EP 03025851
PRIOR FILING DATE: 2003-11-10
PRIOR APPLICATION NUMBER: EP 03013819
PRIOR FILING DATE: 2003-06-18
NUMBER OF SEQ ID NOS: 191
SOFTWARE: Patentin version 3.1
SEQ ID NO 168
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US-60-643-717-18889
                                                                                                                                                                                                                       Matches 118; Conservative
                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                         Best Local Similarity
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233 FFHGIS-IP-----EPEDMETLEEKFSDVHPVALNFWKGCLKMNPDDRLTCSOLLE 282
                    232 TSYPDPKATFPKWSPKNLGELITELDSD----GIDLLQKCLRYYPAERISAKKALDHPYF 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 -SIPE-----PEDM-ETLEEKPSDVHPVALNFWKGCLKWNPDDRLTCSQLLESSYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 555.5; DB 8; Length 300; Pred. No. 1.5e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91; Indels
                                                                                                                                                                                          Sequence 7327, Application US/60643717
GENERAL INFORMATION:
APPLICANT: Abad, Mark S.
TITLE CATT: Abad, Mark S.
TITLE OF THE REFERENCE: 38-21(33629) A
CURRENT APPLICATION NUMBER: US/60/643,717
CURRENT FILING DATE: 2005-01-12
NUMBER OF SEQ ID NOS: 19247
SEQ ID NO 7327
                                                                                                                                                                                                                                                                                                                                                                                                                                       33.4%; Scc... 37.3%; Pred. No. ... 72; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: April 22, 2005, 07:09:11
Job time : 15.2749 secs
                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Pneumocystis carinii
                                                                                                         284 HEYFKDLEMVQ 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 113; Conservative
                                                                     283 SSYFDSFQEAQ 293
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Best Local Similarity
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US-60-643-717-7327
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 19-Dec-1997
C;Accession: S22745
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22222222222222222222222222222222222222	ALI SULT 1 Special kinase (EC 2.7.1.37) cdc2-relat Specials Homo sapiens (man) Accession: \$23383, \$22744 Meyerson, M. Enders G.H.; Wu, C.L.; Meyerson, M. Enders G.H.; Wu, C.L.; Meyerson, M. Enders G.H.; Wu, C.L.; Meyerson, M. Enders G.H.; Wu, C.L.; Meyerson, M. Enders G.H.; Wu, C.L.; Meyerson, M. Enders G.H.; Wu, C.L.; Meyerson, M. Enders G.H.; Wu, C.L.; Accession: \$23383; MJD1:923473 Accession: \$23382; MJD1:923473 Accession: \$23382; MJD1:923473 Accession: \$23382; MJD1:923473 Accession: \$23382; MJD1:923473 Accession: \$23382; MJD1:923473 Accession: \$23382; MJD1:923473 Accession: \$23382; MJD1:923473 Accession: \$1.158 cMEY. Cross-references: UNIPROT:Q00532; EMB Superfamily: kinase-related transform Rejvords: ATP; phosphotransferase; se Rejvords: A	REPLELKFPNI
	kinase (EC 2.7.1.37) 15Oct-1994 #sequence 15Oct-1994 #sequence 15Oct-1994 #sequence 10. \$2338; \$22744 10., \$3338; \$22744 10., \$3338; \$22744 10., \$3338; \$22744 10., \$2338; \$2338; \$338;	242 POPEDMEPLELKFPN. eonine protein kina Homo sapiens (man) -Jan-1995 #sequence
5444 5444 5444 5444 5444 5444 5444 544	RESULT 1 823.383 Protein kinase (EC C;Species: Homo sag C;Date: 15-Oct-1993 C;Accession: \$2338: ERMO J. 11, 2909-238: ERMO J. 11, 2909-238: ERMO J. 11, 2909-238: A;Title: A family c A;Title: A family c A;Title: A family c A;Accession: \$2338: A;Keference number: A;Accession: \$2338: A;Keference 1323 A;Keferences c C;Superfamily: kina C;Superfam	242 eoni Hom
	RESULT 1 S23383 protein kinase (EC 2 C; Species: 18-0ct-1994 C; Accession: S23383; R; Meyerson, M.; Ende RMBO 1.1, 2909-291 A; Title: A family of A; Reference number: A; Accession: S23383 A; Status: nucleic ac A; Accession: S23383 A; Status: nucleic ac A; Accession: S23383 A; Status: nucleic ac A; Accession: Proper mRP A; Residues: 1-79: mRP A; Residues: 1-79: mRP A; Residues: 1-79: mRP A; Residues: 1-79: mRP A; Residues: 1-79; Accession C; Keywords: ATP; phot F; 3-278/Domain: prot F; 3-278/Domain: prot F; 3-28/Domain: prot F; 3-28/Domain: prot F; 3-52,127,129/Acti Dub C; Reywords: ATP; phot F; 3-28/Domain: prot F; 3-52,127,129/Acti Dub C; Reywords: ATP; phot C; Reywords: ATP; pho	Db RESULT 2 S22745 Serine/thr C;Species: C;Date: 13

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A; Molecule type: mRNA
A; Residues: 1-292 < MIC>
A; Cross-references: UNIPROT: P34117; EMBL: L00652; NID: g167695; PIDN: AAA16056.1; PID: g1676:
R; Michaelis, C.; Weeks, G.
Biochim. Biophys. Acta 1179, 117-124, 1993
A; Title: The isolation from a unicellular organism, Dictyostelium discoideum, of a highly
A; Reference number: S39071; MUID: 94032415; PMID: 8218353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Complex: In various organisms, cdc2 has been identified as a component of the M-phase s C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; cell cycle control; phosphoprotein; phosphotransferase; serine/threoninf F;2-254/Domain: protein kinase homology <KIN.
F;10-18/Region: protein kinase ATP-binding motif F;10-18/Region: protein kinase ATP-binding motif F;33,51,126,128/Active site: Lys, Glu, Asp, Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: 840021; 839071
R;Michaelis, C.E.; Weeks, G.
R;Michaelis, C.E.; Weeks, G.
A;Description: The wnicellular organism Dictyostelium discoideum possesses a highly relation: A;Reference number: 840021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein kinase (EC 2.7.1.37) cdc2 homolog - slime mold (Dictyostelium discoideum)
                                                                                                                         ---VESEDDPVVKKIALREIRMLKQ 57
                      PNLVNLIEVFRRKRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 RVLHRDLKPQNLLINRKGELKLADFGLARAFGIPVRTYSHEVVTLWYRAPDVLMGSRKYS 180
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                                                                                             58 LKHPNLVNLIEVFRRKRKRKMHLVFEYCDHTLLNELERNPNG-VADGVIKSVLWQTLQALNF
                                                                                                                                                                                                                                                                                       176 TQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFH
                                                                                                                                                                                                                                                                                                                     CHIHNCIHRDIKPENILITKQGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-18,'Y',20-188,'G',190-292 <MI2>
A;Cross-references: EMBL:L00652
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Matches 115; Conservative
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A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: UNIPROT:Q00526; EMBL:X66357; NID:936612; PIDN:CAA47001.1; PID:936613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Cross-references: GDB:283456
A;Map position: 12q13-12q13
G;Superfamily: kinase-related transforming protein; protein kinase homology
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein
F;2-255/Domain: protein kinase homology <RIN>
F;10-18/Region: protein kinase ATP-binding motif
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
Submitted to the EWBL Data Library, May 1992
A;Reference number: $22743
A;Reference number: $22743
A;Reference sizerial sinary
A;Rolecule type: mRNA
A;Retaus: preliminary
A;Rolecule type: mRNA
A;Residues: 1-376 <MEX>
A;Residues: 1-376 <MEX>
A;Residues: 1-376 <MEX>
A;Residues: 1-376 <MEX>
A;Introns: 152/3; 170/3
C;Supperfamily: kinase-related transforming protein; protein kinase homology
C;Reywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;3-296/Domain: protein kinase homology <KIN>
F;11-19/Region: protein kinase ATP-binding motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 ATRWYRAPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLITRTLGKLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 18-Jun-1993 #sequence_revision 18-Jun-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 376;
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                                                                                                                                                                                                                                                                                                                                                                                                         41; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: S23382; S22743

R; Meyerson, M.; Enders, G.H.; Wu, C.L.; Su, L.K.; Gorka, EMBO J. 11, 2309-2917, 1992
A; Title: A family of human cdc2-related protein kinases
A; Reference number: S23382; MUID:92347325; PMID:1639063
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 67.6%; Pred. No. 1.2e-47; Matches 211; Conservative 41; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.0%; Score 581; DB 2;
39.8%; Pred. No. 1.9e-20;
live 66; Mismatches 96,
                                                                                                                                                                                                                                                                                                                                                    Score 1175.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein kinase (EC 2.7.1.37) cdk3 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Accession: S23382
A,Status: nucleic acid sequence not shown
A,Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                    70.78;
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302 HHPYFENIREIE 313
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Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-305 <MEY>
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Dev. Growth Differ. 35, 647-654, 1993
A; Title: Isolation and characterization of goldfish cdc2, a catalytic component of matura
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C;Superfamily: kinase-related transforming protein; protein kinase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 VGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNG 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233 FFHGIS-IP-----EPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRLTCSQLLE 282
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C;Species: Carassius auratus (goldfish)
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: ISO474
E;Kajiura, H:; Yamashita, M:; Katsu, Y:; Nagahama, Y.
                                                                                                            transforming protein; protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
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                                                                                                                                                                                                                                                                         Query Match 34.4%; Score 571.5; DB 2; Length 294; Best Local Similarity 37.6%; Pred. No. 5.1e-20; Matches 117; Conservative 67; Mismatches 92; Indels 35.
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-294 <CCL).
A;Cross-references: GB:M60526
C;Superfamily: kinase-related transforming protein; protein kinase
C;Superfamily: kinase-related transforming protein; protein kinase
F;2-256/Domain: protein kinase homology <KIN>
F;0-18/Region: protein kinase homology <KIN>
F;10-18/Region: protein kinase ArP-binding motif
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
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P2-256/Domain: protein kinase homology <KIN>
F:10-18/Region: protein kinase ATP-binding motif
F:33,51,128,130/Active site: Lys, Glu, Asp, Lys #status predicted
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34.3%; Score 570.5; DB 1.

Best Local Similarity 38.6%; Pred. No. 5.8e-20;

Matches 120; Conservative 68; Mismatches 90.
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A.Molecule type: mRNA
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C;Species: Zea may8 (maize)
C;Species: Zea may8 (maize)
C;Date: 14-Feb-1992 #text_change 28-Feb-1997
C;Accession: B4044
R;Colasanti, J: Tyers, M.; Sundaresan, V.
Proc. Natl. Acad. Sci. U.S.A. 88, 3377-3381, 1991
A;Title: Isolation and characterization of cDNA clones encoding a functional p34(cdc2)
A;Reference number: A40444; MUID:91195354; PMID:2014258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            encoding a functional p34 (cdc2)
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                                                                                                                     173 VGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNG 232
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C;Species: Zea mays (maize)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Superfamily: kinase-related transforming protein; protein kinase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 34.4%; Score 571.5; DB 1; Length 294; Best Local Similarity 37.9%; Pred. No. 5.1e-20; Matches 118; Conservative 66; Mismatches 92; Indels 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Kerwords: ATP; phosphotransferase
;2-256/Domain: protein kinase homology <KIN>
;10-18/Region: protein kinase ATP-binding motif
;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: A4044
R;Colasanti, J; Tyers, M.; Sundaresan, V.
Proc. Natl. Acad. Sci. U.S.A. 88, 3377-3381, 1991
A;Title: Isolation and characterization of cDNA clones e A;Reference number: A40444; MUID:91195354; PMID:2014258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Residues: 1-294 <COL>
Cross-references: GB:M60526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 SSYFDSFQEAQ 293
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                                                                                                                                         241 VHPAHQLSSIVHG
                                                                                                                                                                                               284 SYFDSFQ 290
                                                                                                                                                                                                                                                283 PYFDGLE 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: A40444
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A;Accession: A41227
A;Molecule type: mRNA
A;Residues: 1-238 AKIN>
A;Coss-references: UNIPROT:P24941; GB:M68520; NID:g180177; PIDN:AAA35667.1; PID:g180178
B;Tsai, L.H.; Harlow, E.; Meyerson, M.
A;Cross-references: UNIPROT:P24941; GB:M68520; NID:g180177; PIDN:AAA35667.1; PID:g180178
B;Tsai, L.H.; Harlow, E.; Meyerson, M.
A;Title: Isolation of the human cdk2 gene that encodes the cyclin A- and adenovirus E1A-6
A;Accession: S17873
A;Title: Isolation of the human cdk2 gene that encodes the cyclin A- and adenovirus E1A-6
A;Accession: S17873
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-298 <TSA>
A;Cross-references: GB:X62071; NID:g312802; PIDN:CAA43985.1; PID:g312803
B;Elledge, S.J.; Spottswood, M.R.
B;Elledge, S.J.; Spottswood, M.R.
B;Elledge, S.J.; Spottswood, M.R.
A;Title: A new human p34 protein kinase, CDK2, identified by complementation of a cdc28 n
A;Tocssion: S16520; MUID:91330891; PMID:1714386
A;Accession: S16520
A;Accession: S16520
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N;Alternate names: cell division control protein CDC2 homolog Eg1
C;Species: Xenopus laevis (African clawed frog)
C;Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004
C;Accession: A37871; S15666; I51662; 314410
R;Paris, J; Le Guellec, R.; Couturier, A.; Le Guellec, K.; Omilli, F.; Camonis, J.; Mach
Proc. Natl. Acad, Sci. U.S.A. 88, 1039-1043, 1991
A;Title: Cloning by differential screening of a Xenopus cDNA coding for a protein highly
                                        Rivinomiya-Tsuji, J.; Nomoto, S.; Yasuda, H.; Reed, S.I.; Matsumoto, K. Proc. Natl. Acad. Sci. U.S.A. 88, 9006-9010, 1991
A;Title: Cloning of a human cDNA encoding a CDC2-related kinase by complementation A;Reference number: A41227; MUID:92020980; PMID:1717994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Map position: 12q3-12q13
C; Superfamily: kinase-related transforming protein; protein kinase homology
C; Superfamily: kinase-related transforming protein; protein kinase homology
C; Keywords: ATP; cell cycle control; mitosis; phosphoprotein; phosphotransferase;
F; 2-255/Domain: protein kinase homology «KIN»
F; 10-18/Region: protein kinase ATP-binding motif
F; 14, 160/Binding site: phosphate (Thr) (covalent) #status predicted
F; 15/Binding site: phosphate (Tyr) (covalent) #status predicted
F; 13, 51, 127, 129/Active site: Lys, Glu, Asp, Lys #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-176, S', 178-298 <ELL>
A.Cross-references: EMBL:X61622; NID:g29848; PIDN:CAA43807.1; PID:g29849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GDB:128984; OMIM:116953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local'Similarity 40.09
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: GDB: CDK2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secaration kinase (EC 2.7.1.37) cdc2 homolog 1 - rice
CiSpecies: Oryza sativa (rice)
CiSpecies: Oryza sativa (rice)
CiSpecies: Oryza sativa (rice)
CiDate: 13-Jan-1995 #text_change 09-Jul-2004
CiAccession: S22440
Ridashimoto, J: Hirabayashi, T.; Hayano, Y.; Hata, S.; Ohashi, Y.; Suzuka, I.; Utsugi, Nol. Gen. Genet. 233, 10-16, 1992
A/Title: Isolation and characterization of cDNA clones encoding cdc2 homologues from Ory
A/Reference number: S22440; MUID:92293101; PMID:1376401
A/Residues: 1-294 cHAS>
A/Residues: 1-294 cHAS>
A/Residues: 1-294 cHAS>
A/Residues: 1-294 cHAS>
A/Cross-references: UNIPROT:P29618; EMBL:X60374; NID:920342; PIDN:CAA42922.1; PID:g20343
C; Superfamily: kinase-related transforming protein, kinase homology
C; Superfamily: kinase-related transforming protein, kinase homology
C; Keywords: ATP: phosphoprotein; phosphotransferase; serine/threonine-specific protein k
F; 2-256/Domain: protein kinase ATP-binding motif
F; 2-256/Domain: protein kinase ATP-binding motif
F; 1127,1129/Active site: Lys, Lys #status predicted
:| : ||:||:|| : ||:|| | :||: | |::||: | ||:|| | ||| ||::||::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::
                                                                                                                                                                                                                                                                                                                                   227 IF---KSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRLTGSQLLES 283
                                                                                                                                                                                                                                                                                                                                                                                                         | :: | :: | : | : | : | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNG 232
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N'Alternate names: Eg1 homolog; protein kinase p34
C;Species: Homo sapiens (man)
C;Date: 17-Jul-1992 #sequence revision 17-Jul-1992 #text_change 09-Jul-2004
&Accession: A41227; S17873; $15520
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34.2%; Score 568.5; DB 2;
Best Local Similarity 37.6%; Pred. No. 7e-20;
Matches 117; Conservative 67; Mismatches 92;
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PYFDDLDKSTL 295
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Diotein kinase (EC 2.7.1.37) cdc2-A [similarity] - African clawed frog N;Alternate names: maturation-promoting factor p34cdc2 chain A C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Species: A4942-000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: A44349
R;Pickham, K.M.; Meyer, A.N.; Li, J.; Donoghue, D.J.
R;Inze, D.; Ferreira, P.; Hemerly, A.; Van Montagu, M. Blochem. Soc. Trans. 20, 80-84, 1992
A;Title: Control of cell division in plants.
A;Reference number: A48984; MUID:92339744; PMID:1634002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 37.1%
Matches 111; Conservative
                                                                                                                                                              A, Molecule type: nucleic acid
                                                                                                                                                                                    A;Residues: 1-294 <INZ>
A;Experimental source: flower
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A; Residues: 1-294 <HIF>
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                                                                                                                                                                                                                                      A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: mRNA A; Molecule type: Molecule type: Molecule type: Molecule 1-92, RV, 34-297 < LEA> A; Residues: 1-92, RV, 34-227; NID: 664665; PIDN: CAA32443.1; PID: 964666 R; Olive, M.; Theze, N.; Philippe, M.; Le Pennec, J.P.; Lerivray, H. Molecule 1. 194 A; 1994 A; Title: Cloning of the Xenopus laevis cdk2 promoter and functional analysis in oocytes A; Reference number: IS1662; WIID: 95129896; PMID: 7828909
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N;Alternate names: cdc2 protein homolog; CDC2a protein; cell division control prote
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 22-Nov-1993 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S23095; A48984; JQ1337; JQ0967; S18202
R;Imajuku, Y.; Hirayama, T.; Endoh, H.; Oka, A.
FEBS Lett. 304, 73-77, 1992
A;Ftite: Exon-intron organization of the Arabidopsis thaliana protein kinase genes
A;Reference number: S23095; MUID:92316202; PMID:1618302
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A; Reference number: A37871; MUID: 91126051; PMID:1704128
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                                                  A;Molecule type: mRNA
A;Residues: 1-297 <PAR>
A;Crose-references: UNIPROT:P23437; UNIPROT:Q9PSU0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 34.0%; Score 565.5; DB 2 Local Similarity 37.8%; Pred. No. 9.7e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: I51662
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DD
A;Residues: 1-39 <0LI>
                                                                                                                             R;le Guellec, R.
submitted to the EMBL Data Library, January 1989
A;Reference number: $15866
A;Accession: $18866
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                         Accession: A3787
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Gene 105, 159-165, 1991
A;Title: Identification of two cell-cycle-controlling cdc2 gene homologs in Arabidopsis t
A;Reference number: JQ1337; MUID:92039027; PMID:1937013
A;Accession: JQ1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Description: phosphotransferase; protein kinase; required for G1 to S-phase transition; C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein ki P;2-256/Domain: protein kinase homology «KIN» F;10-18/Region: protein kinase ATP-binding motif F;10-18/Region: protein kinase ATP-binding motif F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: The Arabidopsis functional homolog of the p34cdc2 protein kinase. A;Reference number: JQ0967; WUID:93005715; PMID:1840925 A;Accession: JQ0967
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R;Ferreira, P.C.G.; Hemerly, A.S.; Villarroel, R.; Van Montagu, M.; Inze,
Plant Cell 3, 531-540, 1991
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A, Status: preliminary; not compared with conceptual translation
                                                                                                                                                   A;Note: sequence extracted from NCBI backbone (NCBIP:10946
R;Hirayama, T.; Imajuku, Y.; Anai, T.; Matsui, M.; Oka, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Introns: 3/3; 65/2; 105/3; 163/3; 218/2; 247/3; 265/3
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60 HPNIVSLQDVLMQDSRLYLIFEFLSMDLKKYLDSIPPCQFMDSSLVKSYLYQILQGIVFC 119
                                                                                              HIHNCIHRDIKPENILITKQGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGDT 176
                                                                                                                              177 QYGSSVDIWAIGCVFAELLIGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHG 236
                                                                                                                                                                                                                                                                                                                                                                          | | | :: | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
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286 YFDDL-DNOIKK 296
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                                  oocytes
                                                                                                                                                                             PID:9214023
                                                                                                                                                                                                                                         C;Superfamily: kinase-related transforming protein; protein kinase homology C;Keywords: ATP; phosphoprotein; phosphoiransferase; serine/threonine-specific protein F;2-256/Domain: protein kinase homology <KIN> F;10-18/Region: protein kinase ATP-binding motif F;33,51,128,130/Active site: Lys, Glu, Asp, Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: mRNA
A,Residues: 1-297 <KAN>
A,Cross-references: UNIPROT:P39951; EMBL:X60767; NID:957533; PIDN:CAA43177.1; PID:957534
C(superfamily: kinase-related transforming protein; protein kinase homology
C,Superfamily: kinase-related transforming protein; protein kinase homology <KIN>
F;2-256/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif
Aritle: Requirement of mos(Xe) protein kinase for meiotic maturation of Xenopus A, Reference number: A44349; MUID:92318937; PMID:1377775
A, Roceasion: A44349
A, Residues: 1-302 < PIC> A; Residues: 1-302 < PIC> A; Residues: 1-302 < PIC> A; Residues: UNIPROT: P35567; GB:M60680; NID:g214022; PIDN:AAA63561.1; PID: A; Experimental source: oocytes
A; Experimental source: oocytes
A; Note: sequence extracted from NCBI backbone (NCBIN:107682, NCBIP:107683)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNLVNLIEVFRRKRKAHLVFEYCDHTLLNELERNPNG -- VADGVIKSVLWQTLQALNFCH 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 IHNCIHRDIKPENILITKQGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGDTQ 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286
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;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                            33.6%; Score 559; DB 1; Length 302; llarity 36.7%; Pred. No. 2e-19; Conservative 68; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 297;
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33.5%; Score 557; DB 1; Le
Best Local Similarity 39.1%; Pred. No. 2.4e-19;
Matches 122; Conservative 63; Mismatches 95;
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Best Local Similarity
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NyAlternate names: protein T21J18.20
C;Specias: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000
C;Accession: T49271
R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Rudd, submitted to the protein Sequence Database, April 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PNLVNLIEVFRRKRKAHLVFEYCDHTLLNELERNPNGVAD-GVIKSVLWOTLQALNFCHI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 HNCIHRDIKPENILITKQ-GIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGDTQ 177
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1 MDQYEKVEKIGEGTYGVYYKARDKVTNBTIALKKIRLEQEDEGVPSTAIREISLLKEMQH
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NyAlternate names: cell division control protein 2 (CDC2)
CySpecies: Homo sapiens (man)
Cybte: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
CyAccession: A29539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 YGSSVDIWAIGCVFAELLIGQPLWPGKSDVDQLYLIIRTLG------KLIPRHQSI
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A;Introns: 3/3; 67/3; 105/3; 163/3; 218/2; 247/3; 265/3
C;Superfamily: kinase-related transforming protein; protein kinase
                                                                                                                                                                                                                                                                                               A;Residues: 1-294 «RIE»
A;Cross-references: EMBL:AL132963; GSPDB:GN00061; ATSP:T21J1B.20
A;Experimental source: cultivar Columbia; BAC clone T21J18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 33.5%; Score 556.5; DB 2; Length Best Local Similarity 36.8%; Pred. No. 2.5e.19; Matches 110; Conservative 70; Mismatches 94; Indels
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A;Gene: GDB:CDC2
A;Cross-references: GDB:119052; OMIM:116940
A;Cross-references: GDB:119052; OMIM:116940
A;Cross-references: GDB:119052; OMIM:116940
A;Cross-references: Indg21.-106211.
C;Superfamily: kinase-related transforming protein; prosphotransferase; serine c;Superfamily: kinase-related transforming protein; phosphotransferase; serine c;Ze56/Domain: protein kinase homology «KIN»
F;2-256/Domain: protein kinase APP-binding motif
F;10-18/Region: protein kinase APP-binding motif
F;14,161/Binding site: phosphate (Tyr) (covalent) #status predicted
F;15/Binding site: phosphate (Tyr) (covalent) #status predicted
F;15/Binding site: phosphate (Tyr) (covalent) #status predicted
A;MOlecule type: mRNA
A;Residues: 1-297 <LEE>
A;Cross_references: UNIPROT:P06493; GB:X05360; NID:929838; PIDN:CAA28963.1; PID:929839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKF-VESEDDPVVKKIALREIRMLKQLK 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.5%; Score 556; DB 2; Length 297; 39.4%; Pred. No. 2.7e-19; tive 61; Mismatches 96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 39.4%
Matches 123; Conservative
                                                                                                                                                      Accession: A29539
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120 HSRRVLHRDLKPQNLLIDDKGTIKLADFGLARAFGIPIRVYTHEVVTLWYRSPEVLLGSA 179

177 QYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHG 236

60 HPNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNG--VADGVIKSVLWQTLQALNFC 117

8 6 8 6 8 6

29

227 -VWPEVESLQDYKNTFPKWKRGSLASHVKNLDENGLDLLSKMLIYDPAKRISGKMALNHP 285

8 B

Search completed: April 22, 2005, 06:51:40 Job time : 26.6949 secs

285 YFDSFQEAQIKR 296 ||: : |||: 286 YFNDL-DNQIKK 296

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

April 22, 2005, 01:29:40 ; Search time 82.7946 Seconds (without alignments) 1948.255 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-766-691-12 1662 1 MEKYEKLAKTGEGSYGVVFK......RKARNEGRNRRRQQVLPLKS 315

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description	Q6axj9 brachydanio	Oscego mus musculu	Q6qua0 homo sapien	Q66he7 rattus norv		_					Q92772 homo sapien	Q9qyi2 mus musculu	Q9quk0 mus musculu	Q9qyil mus musculu	Q6gmd6 xenopus lae	Q6txh3 rattus norv	Q9p114 homo sapien	Q8ivw4 homo sapien	Q9bmg2 trypanosoma	_	Q9grt9 leishmania	Q8bkr2 mus musculu	Q8b149 mus musculu	Q9jm02 rattus norv	Q9jm01 rattus norv	Q8blf2 mus musculu	mus n	homo	homo		Ospve0 mus musculu
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Score	1209.5	1206	1188.5	1184	1183.5	1035.5	1027.5	1027.5	967.5	958	941.5	930.5	930.5	928	924	919.5	784.5	784.5	781	770	769.5	767.5	764.5	763.5	763.5	759.5	720.5	720.5	720.5	708	702.5
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Q9W6R6 Q7RM49 CDEX HUMAN Q9ZRI HUMAN CCCH DICDI CCCH ZCCH Z Q66.H7 CCC2 CARAU Q713L7 CC21 ORYSA CDC2 ORYJA CDC2 HUMAN CDC2 HUMAN CDC2 HUMAN
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ALIGNMENTS

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25-OCT-2004	-2004	(TrEMBLrel.	28,	Created)	0	(otaba;		
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TRAIN	=Singe	pore local	strair	strain; TISSUE=Embryo;	=Emb	ryo;		
ubMed	=12477	PubMed=12477932; DOI=10.1073/pnas.242603899;	.1073/	pnas.24;	6038	166		
trans	berg F	N.L., Feingo	ld E.,	Feingold E.A., Grouse L.H.,	ë Ľ	H., Derg	e G.G.	
Clausn	er R.I	., Collins	F.S.,	Wagner I	s ':	henmen C	. χ.	chuler G.
ltsch	ul S.E	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	В., В	setow K.F	S	chaefer	C.F.,	Bhat N.K.
łopkin	B R.F.	, Jordan H.	, Mooi	e T., Ma	X S	S.I., Wang J., Hsieh	J., E	sieh F.,
iatch	enko I	, Marusina	Ά.	Parmer A.	Α.,	Rubin G.M.,	M., Hong	
taple	ton M.	, Soares M.1	В., ВС	naldo M.	ц	Casavant	I.	Casavant T.L., Scheetz T.E
Srowns	tein M	Brownstein M.J., Usdin T.B., Toshiyuki S.	Т.В.,	Toshiyuk	i.	S., Carninci	Ci.	,, Carninci P., Prange C.,
aha S	.S., I	odnellano N	.A., I	eters G.	٦.,	Abramson	R.D.,	Mullahy
ювак	S.A.,	Bogak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	, MCKe	rnan K.	Σ.	alek J.A	., Gun	aratne P.
char	da S.	Worley K.C.	., На	.e S., G	rcia	A.M.	ay L.J	., Hulyk
illal	on D.	C., Muzny D.	M., Sc	dergren	E. C.	, Lu X.,	GIPPB	R.A.,
ahey	He	iton E., Ker	ttemar	M., Mac	lan A	., Kodri	gues s	., sanche
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Jones	L	Marra M.A.						
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and mouse	use cī	cDNA sequences.";)
roc.	Natl.	Proc. Natl. Acad. Sci.	U.S.A.		9-16	99:16899-16903 (2002)		
[2]								
SEQUEN	CE FRO	SEQUENCE FROM N.A.						
STRAIN	=Sings	STRAIN=Singapore local strain; TISSUE=Embryo;	strair	1; TISSUE	S=Emb	ryo;		
direct	or MG	Director MGC Project;						
Submit	ted (7	Submitted (AUG-2004) to	the	MBL/Gen	ank/	to the EMBL/GenBank/DDBJ databases	аравев	
EMBL;	BC079	J. BC079506; AAH79506.1;	6.1;	; ;				
	:0002	24; F:ATP D	ulbut	I; IEA.	•	:	-	
	:00046	74; F:prote	in sei	ine/thre	onin	e kinase	activ	ity; IEA.
	: 0004	GO:0004713; F:protein-tyrosine Kinase activity; JEA.	ın-tyı	cosine Ki	nase	activit	Y; LEA	. 6
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InterPro;		IPR011009; Ki	nase	Kinase like.				
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60,770 full-length cDNAs.";
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                                                                                                                                                                                                                               SSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLITRTLGKLIPRHQSIFKSNGFFHGISI 239
                                                                                                                                                                                                                                                                      PEPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRLTCSQLLESSYFDSFQE--AQIKRK 297
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                                                                                                                                                SEQUENCE FROM N.A.
STRANIE-STBL/61/ TISSUE=Testis;
STRANIE-STBL/61/ TISSUE=Testis;
The FANTOM CONSORTIUM
THE RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I all Team;
                                                                                                                                      1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male testis CDNA, RIKEN full-length enriched
library, clone:4933411017 product:cyclin-dependent kinase-like 1
                                                                                                                    3;
                                                                                               DB 2; Length 350;
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STRAIN=CS/BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
Prodom, PD000001, Prot kinase; 1.
SMART; SM00220; S TKC; 1.
SMART; SM00219; TYFKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN 1.
ATP-binding; Kinase; Transferase.
SEQUENCE 350 AA; 40810 MW; 9B04440EE0E38BEI CRC64;
                                                                                             72.8%; Score 1209.5; DB:
69.8%; Pred. No. 1.5e-77;
iive 47; Mismatches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                          298 ARNEGRNRRRQQVLP 312
                                                                                                                Matches 220; Conservative
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RC STRAIN-CSTBL/60; TISSUE-Testis;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Hanagaki T., Hayatsu N., Zawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kohun H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numzaki R., Ohno M.,
RA Asano H., Saski D., Shibata K., Shibata Y., Sakai K.,
RA Sano H., Saski D., Shibata K., Shibata Y., Shiragawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagawa A., Takahashi F., Tanaka T.,
RA Pilma Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Dimitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
B. Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
B. Submitted (JUL-2019) to the EMBL/GenBank/DDBJ databases.
B. GO: GO:0004674; F:protein serine/threonine kinase activity; IEA.
B. GO: GO:0004674; F:protein amino acid phosphorylation; IEA.
B. RIEFPC; IPR000219; Protein amino acid phosphorylation; IEA.
B. RIEFPC; IPR000219; Ser Lhr_pkinase.
B. Rieferpc; IPR0002290; Ser Lhr_pkinase.
B. Rieferpc; IPR000021; For thr Lase:
B. Rahar: SMN0220; Striase; I.
B. RAMRT: SMN0220; Striase; I.
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STRAIN=C57BL/6J; TISSUE=restis;

STRAIN=C99913; PubMed=11076861; DOI=10.1101/gr.152600;

MEDLINE=2059913; PubMed=11076861; DOI=10.1101/gr.152600;

A hibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Korno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41023 MW; 6E9F56C8080F35E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48;
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PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
SROITE; PS00108; PROTEIN KINASE ST; UNKNOWN 1.
SEQUENCE 352 AA; 41023 MW; 6E9F56C9080F95E0
Nature 420:563-573(2002).
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Matches 222; Conservative
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TISSUB-Kidney,

Taraubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

PubMed=12477932; DOI=10.1073/pnas.242603899;

Ratausberg R.L., Feingold B.A., Grouse L.H., Schamen C.M., Schuler G.D.,

Ratausherg R.L., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Perers G.J., Abrameon R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu K., Gibbs R.A.,

Rahes J., Helton E., Ketteman M., Madan A., Rodriques S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
  PEPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRLTCSQLLESSYFDSFQEAQIKRKAR 299
                                                                                                                                       242 PDPEDMEPLELKFPNISYPALGLIKGCLHMDPTERLTCEQLLHHPYFENIREIEDLAKEH 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Raftus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Director MGC Project;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databages.
BMBL, BC081896; AAH81896.1;
InterPro; IPR011009; Kinase like.
InterPro; IPR00719; Prot Kinase.
InterPro; IPR008219; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR001245; Tyr_pkinase.
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352 AA; 40899 MW; DB9CDF5464E66E24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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ProDom; PD00001; Proc_kinase; 1.
SMART; SM00220; S TKc; 1.
SMART; SM0019; TyrKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE_ST; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
Hypothetical protein.
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nes 214; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                    NK 303
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181 PPVDVWAIGCVFAELLSGVPLWPGKSDVDQLYLIRKTLGDLIPRHQQVFSMNQYFSGVKI 240
                                                                                                                                                                                                                     241 PDPEDMETLELKFPNISYSALGFLKGCLHMDPAERLICEQLLQHPYFDSIREVGELTRQH 300
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                                                                                                                                                                                         PEPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRLTCSQLLESSYFDSFQEA----QI
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                                                                                   SSVDIWAIGCVFAELLTGOPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGISI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S. Sherwood J.K., Sherwood A.M., Leithauser B.J., Nickerson D.A.; Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases. EMBL, AYS25548; AAS00095.1; -- HSSP; P24941; 1838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004674; F:Drotein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0016740; F:protein amino acid phosphorylation; IEA.
InterPro; IPR01009; Kinase like.
InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser_thr pkinase.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001245; Tyr pkinase.
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Local Similarity 70.5%; Pred. No. 4.8e-76;
Les 213; Conservative 42; Mismatches 46,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
                                                                                                                                                                                                                                                                                                295 KRKARNEGRNRRRQ----QVLP 312
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301 DKPARKTLRQSRKHLTGLQYLP 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                              121
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PNLVNLIEVFRRKRKAMHLVFEYCDHTLLNELERNPNGVADGVIKSVIMOTLQALNFCHIH 120
                                                                                                                                                                                                                                                                                                                                             1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCIHRDIKPENILITKQGIIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTQYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 SSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 PEPEDMETLEEKFSDVHPVALNFWKGCLKWNPDDRLTCSQLLESSYFDSFQBAQ 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anopheles gambiae str. PEST.

Budaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anopheles Genome Sequencing Consortium,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
Prodom; PD000001; Prot kinase; 1.

SMART; SM00220; S. TKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00101; PROTEIN KINASE ST; 1.

ATP-binding; Serine/threonine-protein kinase; Transferase.

DOMAIN 5 288 ATP (By similarity).

BINDING 34 34 ATP (By similarity).

ACT SITE 127 127 Proton acceptor (By similarity).

SEQUENCE 358 AA; 41834 MW; 88344321F24B77C6 CRC64;
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HSSP; P24941; 1010.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0016740; F:protein kinase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016468; F:protein amino acid phosphorylation; IEA.

InterPro; IPR011009; Kinase like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q708G7; TEMBLEL 26, Created)
01-MAR-2004 (TrEMBLEL 26, Last sequence update)
01-MAR-2004 (TrEMBLEL 26, Last sequence update)
AgCP3044
                                                                                                                                                                                                                                                                 Pred. No. 1.1e-75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; 187000719; Prot Kinase.
InterPro; 187000719; Prot Kinase.
InterPro; 18700069; Prot Kinase.
Prognous, Pronoso, I.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00117; PROTEIN KINASE DOM; 1.
PROSITE; PS00118; PROTEIN KINASE ST; UNKNOWN I.
ATP-binding; Kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=agCG55557; ORFNames=ENSANGG0000012213;
                                                                                                                                                                                                                                            71.2%; Score 1183.5; 71.8%; Pred. No. 1.1e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preliminary data.
EMBL; AAAB01008879; EAA08474.1; -.
                                                                                                                                                                                                                                                             Best Local Similarity 71.8
Matches 211; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                        Query Match
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                                                                                  PNLVNLIEVFRRKRRAHLVFEYCDHTLLNELERNPNGVADGVIKSVLMOTLOALNFCHIH 120
                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                              NCIHRDIKPENILITKQGIIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTQYG 179
                                                                                                                                                                                                                                        180 SSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGISI 239
                                                                                                                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                                                     PEPEDWETLEEKESDVHPVALNFWKGCLKMNPDDRLTCSQLLESSYFDSFQE-AQIKRKA 298
                                                                                                                                                                                                                                                                                                                                           9
                                                           9
        MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: AFP + a protein = ADP + a phosphoprotein. SIMILARITY: Belongs to the Ser/Thr protein kinase family. CDC2/CDKX subfamily.
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SEQUENCE FROM N.A.
MEDLINE=92347325; Pubmed=1639063;
MEYERSON M., Enders G.H., Wu C.-L., Su L.-K., Gorka C., Nelson 'Harlow E., Tasi L.-H.;
Harlow E., Tasi L.-H.;
"A family of human cdc2-related protein kinases.";
EMBO J. 11:2909-2917(1992).
EMBO J. 11:2909-2917(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
05-UTL-2004 (Rel. 4L Last annotation update)
Serine/threonine-protein kinase KKIALRE (EC 2.7.1.37) (Cyclindependent kinase-like 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 AA
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EMBL, X66359, CAA47002.1; JOINED.
HF, S23383, S23383.
HSSP, P24941, 1H00.
Genew, HGNC:1781; CDKL1.
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                                                                                                                                                                                                                                                                                                                                                                                                   RNEGRNRRRQ 308
                                                                                                                                                                                                                                                                                                                                                                                                                                        301 DKPTŘKTLŘÝ 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
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RESULT 5

KKIA HUMAN

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DT 01-APR
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RN MEDLINI

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121

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Gaps

1;

41; Indels

DB 1; Length 358;

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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ENMV9
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                                                                                                                                                                                240
                                                                                                                                                                                                                                PNLVNLIEVFRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                                                                                                    121 NCIHRDIKPENILITKQGIIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTQYGS 180
                                                                                                                                                                                                                                                                  241 EPEDMETLEEKFSD---VHPVALNFMKGCLKMNPDDRLTCSQLLESSYFDSF--QEAQIK 295
                                                                                                                                                                                                                                                                                         257 VPPTLETLEAKMPSRTLANPLMMDFLKKCLDKDPAKRWSCERLATHPYFEDYITKQKEIE 316
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                                                                                  1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                                                                                                                  SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGISIP
                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Nematoda, Chromadorea, Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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WormBase; WESTATI, 1820.258.

WormPep; Y42A5A.4; CE20258.

GO, GO:0005224; F:ATP binding; IEA.

GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

GO; GO:0006468; F:protein amino acid phosphorylation; IEA.

GO; GO:0006468; F:protein amino acid phosphorylation; IEA.

InterPro; IPR00119; Kinase like.

InterPro; IPR001220; Ser thr pkinase.

InterPro; IPR00220; Ser thr pkinase.

InterPro; IPR008211; Ser thr pkinase.

ProDom; PD000001; Prot Kinase; 1.

SMART; SM00220; S-TKC; 1.
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                       DB 2; Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Genome sequence of the nematode C.elegans: A platform for
                                              67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
42402 MW; F23BDB4C5D28A5E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                     Query Match 62.3%; Score 1035.5; DB 2
Best Local Similarity 58.1%; Pred. No. 3.2e-65;
Matches 186; Conservative 62; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                       353 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                       01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last seq.
01-WAX-2004 (TrEMBLrel. 26, Last annot Hypothetical protein Y42A5A.4.
                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                  296 RKARNEGRNRRRQQVLPLKS 315
                                                                                                                                                                                                                                                                                                                                         317 QTITLEQKQTGTRELKPKTS 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL032618; CAB63367.1;
HSSP; P24941; 1H00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            investigating biology.";
Science 282:2012-2018(1998)
                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
367 AA;
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SEQUENCE
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NEDLINEE 20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Lid P.W., Hoskins R.A., Galle R.F., George R.A., Elevis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Bardon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., Namandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu H., Baxendale J., Bayraktaroglu L., Beasley E.M., Benson R.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Benson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Autler H., Cadieu E., Center A., Chandra I., Achery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Achery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Durbin K.J., Evangelista C.C., Perriar B.C., Punn P., Borbin K.J., Evangelista C.C., Ferrac C., Ferriars B.C., Dunn P., Borbin K.J., Evangelista C.C., Ferrac C., Ferriars B., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K., Karleh F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalali M., Malush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Lia Z., Liang Y., Lin Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., Liang Y., Lia Z., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 PVDIWAVGCVYAELLIGEALWPGRSDIDQLYHIRKTLGEFLPRHISIFRTNQFFFGLSIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 SVDIWAIGCVFAELLIGOPLWPGKSDVDOLYLIIRTLGKLIPRHOSIFKSNGFFHGISIP
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6
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota; Diptera, Brachycera, Muscomorpha,
Ephydroides, Drosophilidae, Drosophila.
                                                                                                                                                                                             Query Match 61.8%; Score 1027.5; DB 2; Length Best Local Similarity 58.8%; Pred. No. 1.1e-64; Matches 187; Conservative 59; Mismatches 63; Indels
PROSITE, PS00108, PROTEIN KINASE ST, UNKNOWN 1.
ATP-binding, Hypothetical protein, Kinase, Transferase.
SEQUENCE 353 AA, 40665 MW; 7E32260D9849CAC9 CRC64;
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Last annotation update)
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Nelson D.K., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
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Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.
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EMBL; AE003611; AAF52279.1; -.
HSSP; P24941; 101Q.
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GO: 0000910; P:cytokinesis; IMP.
InterPro; IPR011009; Kinase like.
InterPro; IPR00109; Kinase like.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002291; Ser_thr_pkinase.
InterPro; IPR0069; Pkinase; I.
SWART; SW00220; S_TKC; 1.
PR051TE; PS00107; PROTEIN KINASE ATP; 1.
PR051TE; PS00108; PROTEIN KINASE DOM; 1.
PR051TE; PS00108; PROTEIN KINASE ST; UNKNOWN I.
PROFILE PEDINGING; KINASE ST; UNKNOWN I.
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61 PNLVNLIEVFRRKRKKKMILVFEYCDHTLLINELERNPNGVADGVIKSVLWOTLQALNFCHIH 120
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS001108; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Sexine/threonine-protein kinase; Transferase.

SEQUENCE 566 AA; 64052 MW; 5D57595550902EA9 CRC64;
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GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
InterPro; IPR011009; Kinase like.
InterPro; IPR000219; Prot kinase.
InterPro; IPR000219; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
Pfam. PP00069: Pkinase.
               Length 392;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                         .3e-64;
61.8%; Score 1027.5;
58.4%; Pred. No. 1.3e
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ProDom; PD000001; Prot_kinase; 1.
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                                                                                   Matches 184; Conservative
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61 PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
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A Taglienti C.A., Wysk M., Davis R.J.;

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I. Oncogene 13:2563-2574(1996).

I. Oncogene 13:2563-2574(1996).

R. Shillarit's Belongs to the Ser/Thr protein kinase family.

R. Shillarit's Belongs to the Ser/Thr protein kinase family.

R. Shillarit's Belongs to the Ser/Thr protein kinase family.

R. GO:0004672; F:protein kinase activity; TAS.

GO:0004672; F:protein kinase activity; TAS.

GO:0004672; F:protein kinase activity; TAS.

R. GO:0004672; F:protein kinase; 1.

R. Prodom; Pro0069; Prot. Linase; 1.

R. Prodom; Pro0069; Prot. Linase; 1.

R. PROSITE; PS0010; PROTEIN KINASE D9W; 1.

R. PROSITE; PS0010; PROTEIN KINASE ST; 1.

R. PROSITE; PS0010; PROTEIN KINASE ST; 1.

R. PROSITE; PS0010; PROTEIN KINASE ST; 1.

R. ATP-binding; Kinase; Seriale(threonine-protein kinase; Transferase.)

SEQUENCE 493 AA; 56018 MW; 5CC20A91CBF89EFE CRC64;
                                                                             VDIWAIGCVFAELLTGOPLWPGKSDVDQLYLIIRTLGKLIPRHOSIFKSNGFFHG--ISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                  PEPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRLTCSQLLESSYFDSF 289
                                                                                                                                                                      244 TSPRERVPIEALYPKAPSHTISFLKNCLQMDPTWRLDCVELLDHAYFDRY 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IndelB
                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l.9e-58;
nes 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.6%; Score 941.5;
53.1%; Pred. No. 1.9e
:ive 68; Mismatches
                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                      01-FEB-1997 (TrEMBLrel. 02, 01-MAR-2004 (TrEMBLrel. 26, P56 KKIAMRE protein kinase.
                                                                                                                                                                                                                                                                                                                   01-FEB-1997 (TrEMBLrel. 02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                    · PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                               (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 172; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                            Name=KKIAMRE;
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
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                                                                                                                                                                                                                                                 RESULT 11
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                                                         PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                                              121 NCIHRDIKPENILITKQGIIKICDFGFAQIL-IPGDAYIDYVATRWYRAPELLVGDTQYG 179
                                                                                                                                                                                       180 SSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGISI 239
                                                                                                                                                                                                                                                                240 PEPEDMETLEEKFSDVHPVALNFMKGCLKMNPDDRLFCSQLLESSYF--DSF----QEA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIHN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
 MEKYENLGLVGEGSYGMVMKCRNKDSGRIVAIKKFLESDDDKMVKKIAMREIKLLKQLRH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=15343333; DOI=10.1038/nature02709; Seo H.C., Edvardsen R.B., Maeland A.D., Bjordal M., Jensen M.F., Hansen A., Flaat M., Weissenbach J., Lehrach H., Wincker P., Reinhardt R., Chourzout D.; "Hox cluster disintegration with persistent anteroposterior order."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.6%; Score 958; DB 2; Length 385; 57.9%; Pred. No. 1e-59; ive 58; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oikopleura dioica.
Eukaryota, Metazoa, Chordata, Urochordata, Appendicularia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             385 AA; 45512 MW; 059F814421A6ADA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Cyclin-dependent kinase-like 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AY449462; AAS21447.1; -... GO; GO:0016301; F:kinase activity; IEA. InterPro; IPR011009; Kinase like. InterPro; IPR000719; Prot Kinase. InterPro; IPR0002290; Ser Ihr pkinase. InterPro; IPR008271; Ser thr pkinase. InterPro; IPR001245; Tyr pkinase.
                                                                                                                                                                                                                                                                                                                                        QIK--RKARN-----EGRNRRQQ 309
                                                                                                                                                                                                                                                                                                                                                             | : | : | | | : | | | OMKVQKDARNISLSKKSQNRKKEK 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression in Oikopleura dioica.";
Nature 431:67-71(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00069; Pkinase; I.
ProDom; PD000001; Prot kinase; I.
SMART; SM00220; S_TKC; I.
SMART; SM00219; TYrKC; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oikopleuridae; Oikopleura.
NCBI_TaxID=34765;
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Matches 168; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PNLVNLIEVFRRKRKMHLVFEYCDHTLINELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 NCIHRDIKPENILITKQGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGDTQYG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGISI 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 PEPEDMET--LEEKFSDVHPVALNFWKGCLKMNPDDRLTCSQLLESSYF--DSF----Q 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CSTRAIN-CSTBL/6; TISSUE-Brain;
Sassa T., Gomi H., Sun W., Ikeda T., Thompson R.F., Itohara S.;
Submitted (UNN-1999) to the EMBL/GenBank/DDBJ databases.

C. 1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

EMBL; AB029066; BAA88428.1; -.

R HSSP; P24941; 1010.

GO; GO:0005524; F:APP binding; IEA.

GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR00109; Kinase like.

InterPro; IPR00109; Kinase like.

InterPro; IPR00209; S=Thr pkinase.

InterPro; IPR00220; S=Thr pkinase.

R Probom; PD0000001; Prot kinase; I.

R Probom; PD0000001; Prot kinase; I.

R Probom; PD0000001; STRC: Linase; I.
                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00220; S. TKC; I.
PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS500119; PROTEIN KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN KINASE_ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 564 AA; 63640 MW; DACDEF630CCE82D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.0%; Score 930.5; DB 2; Length 564; 53.4%; Pred. No. 1.3e-57; ive 66; Mismatches 69; Indels 17;
                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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ELQLKIEKDARNNSLPKKSQNRKKEK 326
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                              301 QLKVQKDARNVSLSKKSQNRKKEK 324
                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                            01-MAY-2000 (TYEMBLrel. 13, C
01-MAY-2000 (TYEMBLrel. 13, L
01-OCT-2003 (TYEMBLrel. 25, L
Ser/Thr kinase KKIAMRE-gamma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 53.4%
Matches 174; Conservative
                                                                                                                                                                                                                                                                                                       Name=Cdkl2; Synonyme=Kkm;
                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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61 PNLVNLIEVFRRKRKRKHLVFEYCDHTLLNELERNPNGVADGVIKSVLWGTLQALNFCHIH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 PEPEDMET--LEEKFSDVHPVALNFMKGCLKWNPDDRLTCSQLLESSYF--DSF----Q 290
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Probon; PD00001; Proc kinase; 1.
SWART; SM00220; S_TKC; 1.
SWART; SM00220; S_TKC; 1.
PROSITE; PS00101; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Serine/threonine-protein Kinase; Transferase.
SEQUENCE 568 AA; 64055 WW; A43B75E2E9EB86C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:1858227; Cdkl2.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004524; F:ATP binding; IEA.

GO; GO:000464; F:protein serine/threonine kinase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR011009; Kinase like.

InterPro; IPR000719; Fort Kinase.

InterPro; IPR002290; Ser thr_pkinase.

InterPro; IPR00659; Pkinase; I.

Pfam; PF00069; Pkinase; I.
                                                                                                                                                                                                                                                                                                                         STRAIN=129/SvJ, and C57BL/6; TISSUE=brain, Sassa T., Gomi H., Sun W., Ikeda T., Thompson R.F., Itohara Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.0%; Score 930.5; DB 2; Length 53.4%; Pred. No. 1.4e-57; ative 66; Mismatches 69; Indels
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
02-UJL-2004 (TrEMBLrel. 27, Last annotation update)
Ser/Thr kinase KKIAMRE (Ser/Thr kinase KKIAMRE)
Name=Cdkl2; Synonyms=Kkm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EAQIK--RKARN----EGRNRRRQO 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB029073; BAA88439.1; CR SELL; AB029068; BAA88439.1; CINED. EMBL; AB029069; BAA88439.1; JOINED. EMBL; AB029070; BAA88439.1; JOINED. EMBL; AB029072; BAA88439.1; JOINED. EMBL; AB029072; BAA88439.1; JOINED. EMBL; AB029065; BAA88439.1; JOINED. EMBL; AB029065; BAA88439.1; JOINED. EMBL; AB029065; BAA88427.1; CINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 53.48
Matches 174; Conservative
                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                               MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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090Y11

RESULT 14

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TISSUB-Kidney,

WEDLINE-22188257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Straubberg R.L., Fefigodd B.A., Grouse L.H., Derge J.G.,

Ratusberg R.L., Zeeberg B., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

Datchenko L., Marusina K.F., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Male M. Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rotiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

"Month R. M. Madan A., Peters R. M., Bouffard G.G.,

And Montes China and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probom; PD000001; Prot kinase; 1.
SWART; SW00210; S_TKC; 1.
SWART; SW00219; TyrKC; 1.
PROSITE; PS00101; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=Kidney;
BEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOC443693 protein (Fragment).
Name=LOC443693.
Kenopus laevis (African clawed frog).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostc Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37063 MW; 4CD2189603F9115F CRC64;
                                      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR011005; Kinase like.
InterPro; IPR001019; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR008271; Ser thr pkinase.
InterPro; IPR001245; Tyr pkinase.
                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00069; Pkinase;
                                                                                                                                                                                           Kenopodinae; Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Kidney;
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                             NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               initiative."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
61 PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCIHRDIKPENILITKQGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGDTQYG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNGFFHGISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEPEDMET--LEEKFSDVHPVALNFWKGCLKMNPDDRLTCSQLLESSYF--DSF----Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00069; PKinase; I.
Probom; PR00001; Prot kinase; I.
PROSITE; PS00107; PROTEIN KINASE ATP; I.
PROSITE; PS00101; PROTEIN KINASE DOM; I.
ATP-binding; PROTEIN KINASE ST; I.
ATP-binding; Riase; Serine/threonine-protein kinase; Transferase.
NON_TER
                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUB=Brain;
SASSA T. Gomi H., Sun W., Ikeda T., Thompson R.F., Itohara S.;
Submitted (JUN-1999) to the EMBL/Genbank/DDBJ databases.
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; AB029067; BAA88429.1; -.
HSSP; P24941; IOIQ.
MCD; MCI:1858227; Cdkl2.
GO; GO:0005524; F:ATP binding; IBA.
GO; GO:0005524; F:protein serine/threonine kinase activity; IEA.
GO; GO:0016740; F:protein amino acid phosphorylation; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR011009; Kinase.
InterPro; IPR00719; Prot kinase.
InterPro; IPR002290; Ser thr pkinase.
InterPro; IPR008271; Ser thr pkinase.
Finam: PF0006971; Ser thr pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 AA; 38023 MW; F72EB89E65AE8585 CRC64;
                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55.8%; Score 928; DB 2;
53.9%; Pred. No. 1.1e-57;
iive 63; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 AA.
                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Last sequent
01-OCT-2003 (TrEMBLrel. 25, Last annotat
Ser/Thr kinase KKIAMRE-delta (Fragment)
                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | |:| : || | ELOLKI EKDARNNSLPKKSOK 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 53.9% les 173; Conservative
                                                                                                                                                                                     Name=Cdk12; Synonyms=Kkm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                          PRELIMINARY;
                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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Query Match

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Q6GMD6 RESULT 15 Q6GMD6 ID Q6GMD

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61 PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                                  180 SSVDIWAIGCVFAELLIGQPLWPGKSDVDQLYLLIRTLGKLIPRHQSIFKSNGFFHGISI 239
                                                                                                                                                                                                  181 KAVDVWAIGCIVTEMLTAQPLFPGDSDIDQLHHIIKCQGNLTPRHQELFYRNPMFAGVSL 240
                                                                                                                                                                                                                                                  PEPEDMETLEEKFSDVHPVALNFWKGCLKMNPDDRLTCSQLLESSYF--DSFQE---AQI 294
                                    1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH 60
                                                                 9
                                                   6; Gaps
Best Local Similarity 53.8%; Pred. No. 2.1e-57;
Matches 169; Conservative 64; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                    KRKARNEGRNRRRQ 308
                                                                                                                                                                                                                                                                                                  : | :| : |
301 RAKLQNLSKDNSSQ 314
                                                                                                                                                                                                                                    240
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Search completed: April 22, 2005, 06:50:40 Job time : 83.7946 secs

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5.1.6
Compugen Ltd.
 GenCore version
Copyright (c) 1993 - 2005
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OM protein - protein search, using sw model

April 22, 2005, 01:23:15; Search time 96.4471 Seconds (without alignments) 1391.497 Million cell updates/sec Run on:

1 MEKYEKLAKTGEGSYGVVFK.....RKARNEGRNRRRQQVLPLKS 347 US-10-766-691-10 1820 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 Total number of hits satisfying chosen parameters:

2105692 segs, 386760381 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 16Dec04:* 1: geneseqp1980s:* Database

geneseqp2003as:* geneseqp2003bs:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	;	kin	_	kin	kin	kin	pro	pro	MAR	pol		kin		MAR	phil	MDD	t K	162	uro					kin	108	RE d
	Б Б	Human	Human	Human	Human	Human	Human	Novel	Mouse	Human	Нишап	Нишап	Novel	Human	Drosophi]	Human MDD	Rabbit	Human	Human urc	Human	Human	Human	Нишап	Нишап	Human	NKIAMRE d
	Description	Aae00494	Aae00491	Aae00495	Aae19152	Aae00492	Aau03525	Aab65643	Adi29250	Abp62954	Ado01538	Aag78547	Aab65642	Adi29249	Abb63118	Abu11689	Aay90724	Adc77659	Adq89156	Abp96087	Adi40875	Aae00490	Aae00493	Adk71868	Aay70126	Adi57233
	ΩI	AAE00494	AAE00491	AAE00495	AAE19152	AAE00492	AAU03525	AAB65643	AD129250	ABP62954	AD001538	AAG78547	AAB65642	ADI29249	ABB63118	ABU11689	AAY90724	ADC77659	ADQ89156	ABP96087	ADI40875	AAE00490	AAE00493	ADK71868	AAY70126	AD157233
	DB	4	4	4	ហ	4	4	4	ω	ഗ	8	'n	4	8	₹	9	ო	7	œ	9	œ	4	4	œ	٣	œ
	Length DB	347	356	315	342	324	360	296	296	358	358	228	247	247	392	197	995	493	493	362	183	187	198	205	455	455
de	Query Match	100.0	98.7	89.9	88.6	88.6	87.5	69.8	69.8	63.9	63.6	62.3	61.7	61.7	55.0	52.1	51.7	50.3	50.3	50.1	45.6	43.5	43.5	43.5	41.7	41.7
	Score	1820	1796	1636	1613	1612	1593	1270.5	1270.5	1162.5	1157.5	1134	1123	1123	1001.5	948	941.5	915.5	915.5	911.5	829.5	791	791	791	758.5	758.5
	Result No.	-	8	m	4	ß	φ	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

55 8 AD157214 55 8 AD157236 57 3 AAV70125 57 3 AAV70125 58 6 ABW3922 58 6 ABW3922 58 8 AD89222 59 8 AD157200 59 7 AD68738 50 8 AD157200 50 8 AD157200 50 8 AD157200 50 8 AD157200 50 8 AD157200 50 8 AD157200 50 8 AD157200 50 8 AD157200 50 8 AD157200 50 8 AD187200 50 8 AD157200 50 8 A	2 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	Adi57214 Human NKI Adi57236 CDK3 domi Adu03524 Human pro Aay70125 Rat 108t Aby70125 Rat 108t Abu05290 Human dia Abb65645 Novel pro Adi2925 Human MAR Abg66142 Novel hum Adf68738 Human kin Adf68738 Human kin Adf68738 Human kin Adi57200 Human CDK Adi57237 CDK3 domi Aaw85028 CDK2-aree	4404
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		ADI57214 ADI57236 AAU03524 AAX70125 AAX70124 AAX70124 ABM83922 ABM83922 AABE5645 ADI29252 ABG66142 ADI87200 ADIS7237 ADIS7237 ADIS7237 ADM35028	AAM41062 AAW95689 AAW85029 ADD21390
		00000000000000000000000000000000000000	552 98 44 28 7 7
44444468888888888888888888888888888888		7588.7 7388.7 7388.5 713.7 713.7 73.7 73.7 73.7 73.7 73.7 73	558 557 557 556
•	7588.7 7388.7 73.7 73.7.1 73.7.1 73.7.1 73.7 73.7 7	0 C C C C C C C C C C C C C C C C C C C	. 4 4 4 4 1 5 6 6 7 8

ALIGNMENTS

Human; kinase; gene therapy; bioreactor; mental disorder; biological disorder. AAE00494 standard; protein; 347 AA (first entry) Human kinase #5. WO200123579-A1. Homo sapiens. 19-JUN-2001 05-APR-2001. AAE00494; AAE00494

27-SEP-2000; 2000WO-US026621.

(LEXI-) LEXICON GENETICS INC.

28-SEP-1999; 99US-0156511P.

Friedrich G, Turner CA, Nehls M, Donoho G, Sande AT;

'n

Zambrowicz

WPI; 2001-266166/27. N-PSDB; AAD03816.

New isolated human kinase polynucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases.

Claim 2; Page 32-33; 38pp; English.

The present sequence is novel human protein (NHP) known as human kinase. The human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the identification of other cellular gene products related to human kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical

antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases.

Disclosure; Page 28-29; 38pp; English.

us-10-766-691-10.rag

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probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP products are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression
                                                                                                                                                                                                                                                                    PNLVNLIEVFRRRRRRWHLVPEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                                                                                                                                                                                                                                   180
                                                                                                                                                                                                                                                                                                                                                   240
                                                                                                                                                                                                                                                                                                                                                                PNLVNLIEVFRKKKKMHLVFEYCDHTLINELERNPNGVADGVIKSVIMQTLQALNFCHIH 120
                                                                                                                                                                                                                                                                                                               VASQSAGIIGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFWKGCLK 300
                                                                                                                                                                                                                                                                                                                                                                                                VASQSAGITGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCLK 300
                                                                                                                                                                                                     9
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                                                                                                                                                                                                                      MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                                                                                                                                                                                                                                                 SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA
                                                                                                                                                                                                MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALRETRMLKQLKH
                                                                                                                                                                                                                                                                                                 NCIHRDIKPENILITKQGIIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTQYGS
                                                                                                                                                                           Gaps
   The labelled NHP
                                                                                                                                                                          ;
0
                                                                                                                                                   Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                MNPDDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQQVLPLKS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
   are used as probes.
                                                                                                                                                Score 1820; DB 4;
Pred. No. 1.6e-186;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE00491 standard; protein; 356 AA
                                                                                                                                     100.0%; Sc.__
100.0%; Pre-
disorders. NHP oligonucleotides
                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 347, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry
                                                                                                                         Sequence 347 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human kinase #2
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therapy for the modulation of NHP expression

Sequence 356 AA;

The present sequence is novel human protein (NHP) known as human kinase. The human kinases share structural similarity with animal kinases, more particularly series or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs of effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in calagnostic assays, for the identification of other cellular gene products related to human kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical isorders. NHP oligonucleotides are used as probes. The labelled NHP probe probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP products are used to genetically engineer cells in vivo that functions as body. Nucleotide constructs are used to genetically engineer cells in vivo that functions as body. Nucleotide constructs are used in gene therapy for the modulation of an open of the paramy for the modulations.

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                                                                                                                                                                               NCIHRDIKPENILITKQGIIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTQYGS
                                                                                                                                                                                                                                                                                          1 MEKYEKLAKTGEGSYGVVFKCRNKTSGOVVAVKKFVESEDDPVVKKIALBEIRMLKOLKH
                                                                                                           PNLVNLIEVFRRKRKMHLVFEYCDHTLINELERNPNGVADGVIKSVLWQTLQALNFCHIH
                                                                                                                                                                                                                    SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA
                                                                                                                                                                                                                                     SVDIWAIGCVFAELLIGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA
                                                       MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                                                                NCIHRDIKPENILITKQGIIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTQYGS
                               Gaps
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    Length 356;
 98.7%; Score 1796; DB 4; Length 3 100.0%; Pred. No. 6.5e-184; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; kinase; gene therapy; bioreactor; mental disorder; biological disorder.
                                                                                                                                                                                                                                                                                                                                342
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                                                                                                                                                                                                                                                                                                                                                                                                                          AAE00495 standard; protein; 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
Query Match
Best Local Similarity 100.
Matches 342; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human kinase #6.
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BXSXEXXEX
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Human; kinase; gene therapy; bioreactor; mental disorder; biological disorder.

New isolated human kinase polynucleotide useful for generating

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Zambrowicz

Friedrich G,

Nehls M,

Turner CA,

Donoho G, Sands AT;

WPI; 2001-266166/27.

N-PSDB; AAD03813

27-SEP-2000; 2000WO-US026621

WO2001235.79-A1

05-APR-2001

Homo sapiens

99US-0156511P

28-SEP-1999;

(LEXI-) LEXICON GENETICS INC

us-10-766-691-10.rag

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The present sequence is novel human protein (NHP) known as human kinase.

The human kinases share structural similarity with animal kinases, more particularly series or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase cDNA is disease, and also as a therapeutic. It is useful for screening of disease, and also as a therapeutic. It is useful for screening drugs of effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagants in classocial assays, for the identification of other cellular gene products related to human kinases, and as reagents in sassays for screening compounds that are useful for treating metal, biological or medical disorders. NHP oligonucleotides are used as probes. The labelled NHP copolymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in the products are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene
                                                                                                                                                                                                                                                                                                                                  New isolated human kinase polynucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases.
                                                                                                                                                                                                    Zambrowicz B;
                                                                                                                                                                                                    Turner CA, Nehls M, Friedrich G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapy for the modulation of NHP expression
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 33-34; 38pp; English.
                                                                 27-SEP-2000; 2000WO-US026621.
                                                                                                           99US-0156511P
                                                                                                                                                        (LEXI-) LEXICON GENETICS INC
                                                                                                                                                                                                                                                                     WPI; 2001-266166/27.
                                                                                                                                                                                                                                                                                           N-PSDB; AAD03817.
                                                                                                           28-SEP-1999;
                                                                                                                                                                                                    Jonoho G,
                                                                                                                                                                                                                           Sands AT;
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Sequence 315 AA;

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PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                                                                                                              PNLVNLIEVFRRKRKAHLVFEYCDHTLINELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                                                                                                                                                                 121 NCIHRDIKPENILITKQGIIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTQYGS 180
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                                                                                                 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH 60
                                                                             1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH 60
                                      0; Indels 32; Gaps
89.9%; Score 1636; DB 4; Length 315; 90.8%; Pred. No. 9e-167;
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                                    0; Mismatches
                                        Conservative
  Query Match
Best Local Similarity
                                    Matches 315;
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The present invention relates to an isolated human kinase polypeptide (PKIN) or a biologically active/immunogenic fragment of PKIN is useful for diagnosing, treating and preventing cancer (e.g., leukaemia, lymphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's cardisoase, rheumatoid arthritis), a growth and developmental disorder (e.g., atherosclerosis, hypertension, myocardial infarction), and a lipid disorder (e.g., fatty liver, cholestasis, caucher's disease, Niemann-Pick's disease). PKIN is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. RKIN is useful in a somatic or germinals to model human diseases, in somatic or germine gene therapy, to generate a transcript image of a tissue or cell type, for detecting canimals to model human diseases, in somatic or germine gene therapy, confiferences in the chromosomal location due to translocation, inversion, etc., among normal, carrier or affected individuals, and as hybridisation probes for mapping naturally occurring genomic sequences. PKIN is useful

New human kinase polypeptide, useful in diagnosis, prevention and treatment of cancer, immune disorder, growth and developmental disorder, cardiovascular disorder and lipid disorder.

WPI; 2002-206083/26. N-PSDB; AAD30557.

Claim 1; Page 147-148; 196pp; English

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Thornton M, Yue H, Khan FA, Gururajan R, Hafalia AJA, Walia NK;
Patterson C, Ramkumar J, Gandhi AR, Policky JL, Baughn MR;
Tribouley CM, Bandman D, Nguyen DB, Lu Y, Burford N, Lal P, Ding L;
Yao MG, Elliott VS, Recipon SA, Kearney L, Lu DAM, Greenwald SR;
Tang YT, Xu Y, Walsh RT, Gietzen KJ, Yang J, Hillman JL;
                                                                                                                              Human; kinase polypeptide; PKIN-10; gene therapy; Addison's disease; leukaemia; immune disorder; lymphoma; melanoma; developmental disorder; acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension; asthma; Crohn's disease; rheumatoid arthritis; bursitis; atherosclerosis; cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer; cholestasis; cardiant; cardiovascular disorder; Nieman-Pick's disease; lipid disorder; fatty liver; Gaucher's disease; mycoardial infarction; drug screening; transgenic animal; antiinflammatory; hepatotropic;
                                                                                                                                                                                                                                                                                                                      /note= "Eukaryotic protein kinase domain"
                                                                                                                                                                                                                                                                                         Location/Qualifiers
4. .286
                                                                                                        Human kinase polypeptide (PKIN-10).
                          AAE19152 standard; protein; 342 AA.
                                                                                                                                                                                                                                          hypotensive; anti-HIV; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-2000; 2000US-0220038P.
28-JUL-2000; 2000US-0222112P.
04-AUG-2000; 2000US-0222831P.
11-AUG-2000; 2000US-0224729P.
                                                                                                                                                                                                                                                                                                                                                                                                    20-JUL-2001; 2001WO-US023092
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                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                 WO200208399-A2
                                                                                                                                                                                                                                                                    Homo sapiens
                                                                             21-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                          31-JAN-2002
                                                                                                                                                                                                                                                                                               Key
Domain
RESULT 4
                             CCCCCCCCCCCCCCCX8X4444X88X411111X344X6X6X6X6X6X6X6X6X6X6X6X6X6XX4X4X6
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technologies, in PCR technologies, in dipstick, pin, multiformat enzyme linked immunosorbent (ELISA)-like assays and in microarrays utilising fluids or tissues from patients to detect altered PKIN expression. The present sequence is human PKIN-10
                                                                                                                                                                                                                                         61 PNLVNLIEVFRKKKKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH
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                                                                                                                   Score 1613; DB 5;
Pred. No. 3.1e-164;
1; Mismatches 0;
                                                                                                            Query Match
Best Local Similarity 89.9%;
Matches 312; Conservative
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                                                                                 Sequence 342
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AAE00492 standard; protein; 324 AA
           (first entry)
           19-JUN-2001
       AAE00492;
RESULT 5
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Human; kinase; gene therapy; bioreactor; mental disorder; biological disorder.

Human kinase #3.

WO200123579-A1. Homo sapiens

05-APR-2001

27-SEP-2000; 2000WO-US026621. 28-SEP-1999;

(LEXI-) LEXICON GENETICS INC

Turner CA, Nehls M, Friedrich G, Donoho G, Sands AT;

Zambrowicz

WPI; 2001-266166/27. N-PSDB; AAD03814. New isolated human kinase polynuclectide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases.

WO200138503-A2

31-MAY-2001.

Disclosure; Page 30; 38pp; English.

```
The present sequence is novel human protein (NHP) known as human kinase.

The human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase cDNA is useful for the detection of mutant human kinase cDNA is disease, and also as a therapeutic. It is useful for screening drugs of disease, and also as a therapeutic. It is useful for screening drugs of effective in the treatment of symptomatic or phenotypic manifestations of perturbing the normal function of MHP in the body. The NHP nucleotide sequences are useful for generation of onter cellular gene products related to human kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical disorders. NHP oligonucleotides are used as probes. The labelled NHP probes are useful for screening human genomic library for identifying probes are useful for screening human genomic library for identifying compounds that are useful for screening human genomic library for identifying within the exons, introns and splice sites that can be used in characters and pharmacogenomics. Nucleotide construct encoding NHP brockettes are used to genetically engineer cells in vivo that functions as body. Nucleotide constructs seconding functional NHPs are used in gene body. Nucleotide constructs encoding necessary for the modulation of NHP expression
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metabolic disorder, immune related disease, neurological disorder,
neurodegenerative disorder, inflammatory disorder; infectious disease,
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88.6%; Score 1612; DB 4;
Best Local Similarity 90.6%; Pred. No. 3.6e-164;
Matches 310; Conservative 0; Mismatches 0;
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standard; protein; 296 AA
  AAB65643
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Best Local 8
                                                                                                     Human;
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Matches
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                                                                                                                                                                                                                        AAU03501-AAU03557 represent novel human protein kinases #1-57. The novel protein kinases have been identified as members of the tyrosine or serine/threonine kinase (PTK and STK) families. The polymuclectides coording protein kinases and the polypeptides may be used in the protein kinase and treatment of diseases associated with cancers (especially cancers of haemacropielic origin), cardiovascular cancers (especially cancers of haemacropielic origin), cardiovascular disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), immune related diseases (e.g. rheumatoid arthritis), neurological disease (e.g. sch); only sorders (e.g. asthma), infectious disease (e.g. HIV) and reproductive disorders (e.g. infertility).

Additionally, polymucleotides encoding protein kinases may be used for general therapy and as DNA probes in diagnostic assays. The protein kinase polypeptides may be used as antigens in the production of antibodies against the protein kinase and in assays to identify modulators of protein kinase expression and activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PNLVNLIEVFRKRRAHLVFEYCDHILLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PNLVNLIEVPRRKRKRGHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KFSDVHPVALNFMKGCLKMNPDDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQ-- 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 KFSDVHPVALNFWKGCLKANPDDRLTCSQLLESSYFDSFQEAQIKRKARNBGRNRRRQQN 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----IPGDAYTDYVA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 NCIHRDIKPENILITKOGIIKICDFGFAQILSNSHVGRIDLPDLIDAFAVPGDAYTDYVA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 TRWYRAPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTL---- 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RHVDQAGLELLTSSDPPAVASQSAGITGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEE 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                      preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRWYRAPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52; Gaps
                                                                                                                                                                  diagnosing and/or treating e.g. cancer, immune, cardiovascular and
neuronal-associated diseases, and microbial infections.
                                                                           Martinez R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1593; DB 4; Length 360;
Pred. No. 4.7e-162;
2; Mismatches 0; Indels 52
                                                                                                                                                     Nucleic acids encoding human kinase polypeptides, useful for
                                                                           Sudarsanam S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCIHRDIKPENILITKOGIIKICDFGFAQIL----
                                                                           Manning G,
                                                                                                                                                                                                       Claim 7; Fig 2; 433pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.5%;
22-NOV-2000; 2000WO-US032085
                          99US-0167482P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 85.2
Matches 311; Conservative
                                                                         Whyte D,
Clary D;
                                                                                                                WPI; 2001-343950/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 QVLPL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ÓLLPL 333
                                                  (SUGE-) SUGEN INC
                                                                                                                           N-PSDB; AAS06725
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 360 AA;
                           24-NOV-1999;
                                                                           Plowman GD,
                                                                                        Flanagan P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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RESULT 7

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The present sequence is a novel protein kinase. The novel protein kinases and the nucleic acids that encode them may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and easely. The kinase polypeptides may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies expression and activity biseases related to kinase expression and activity biseases related to kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 KIALREIRMLKQLKHPNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKS 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 VLWQTLQALNFCHIHNCIHRDIKPENILITKQGIIKICDFGFAQILIPGDAYTDYVATRW 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 YRAPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHV 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disorders, complications of organization, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative-trees trees related disorders, chronic inflammatory bowel disease, chronic inflammatory polyic disease, multiple sclerosis, asthma, osteoarthriis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59
                                                                                                                                               protein kinase; antiarthritic; antisclerotic; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 VIMQTLQALNFCHKHNCIHRDVKPENILITKQGMIKICDFGFARILIPGDAYTDYVATRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KIALREIRMLK-LKHPNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVSDGVIKS
                                                                                                                                                                             immunosuppressive; cardiant; renal; antinflammatory; antiasthmatic;
dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
immune disorder; cardiovascular disease; neurodegenerative disease;
cancer; autoimmune disorder; stroke; inflammatory bowel disease;
inflammatory pelvic disease; multiple sclerosis; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
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80.5%; Pred. No. 1.8e-127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sudersanam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurodegenerative diseases and/or cancers.
                                                                       Novel protein kinase, SEQ ID NO: 170.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Whyte D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 10; Fig 1; 310pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAY-2000; 2000WO-US014842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0136503P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plowman GD, Martinez R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-032161/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SUGE-) SUGEN INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VO200073469-A2
                                                                                                                                               mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                       Aus musculus
27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37-DEC-2000
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106 VLWQTLQALNFCHIHNCIHRDIKPENILITKQGIIKICDFGFAQILIFGDAYTDYVATRW 165

60 VLWQTLQALNFCHKHNCIHRDVKPENILITKQGMIKICDFGFARILIPGDAYTDYVATRW 119

166 YRAPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHV 286 DVHPVALNFWKGCLKMNPDDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQ--QVL

172

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226 DQAGLELLTSSDPPAVASQSAGITGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFS

343

KIALREIRMLKQLKHPNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKS 105

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useful for preparing a composition for treating hyperproliferative disorder, particularly cancer and neurodegenerative diseases e.g. Alzheimer's disease. The present sequence is a MARK3 associated protein included in the figures but not mentioned anywhere else in the
                                                                                                                                                                                                                                                                                                                                                                                 Query Match
69.8%; Score 1270.5; DB 8; Length 296;
Best Local Similarity 80.5%; Pred. No. 1.8e-127;
Matches 243; Conservative 19; Mismatches 5; Indels 35;
                                                                                                                                                                                                                                                                                       Sequence 296 AA;
                                                                                                                                                                                             specification
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e,

Gaps

35;

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343
 DQAGLELLISSDPPAVASQSAGITGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFS 285
                               207
                                                                                     267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a compound comprising a sequence comprising 8-80 base pairs (bp) targeted to a nucleic acid encoding MARK3 (MAP/microtubule affinity-regularing kinase 3), that specifically hybridises with the nucleic acid encoding MARK3 and inhibits expression of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a composition comprising the compound and a carrier or diluent, inhibiting the expression of MARK3 in cells or tissues, treating an animal having or suspected of having a disease or condition associated with MARK3 and screening for an antisense compound. The antisense oligonucleotide is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense compound targeted to a nucleic acid molecule encoding microtubule-affinity-regulating kinases (MARK3), useful for modulating expression of MARK3 or for treating cancer or Alzheimer's disease.
                  -----GKLIPRHQSIFRSNQFFRGISIPEPEDMETLEEKFS
                                                    286 DVHPVALNFWKGCLKMNPDDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQ--QVL
                                                                    MAP/microtubule affinity-regulating kinase 3; c. Alzheimer's disease; neurodegenerative disorde; hyperproliferative disorder; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                     MARK3
                                                                                                                                                                                                                                                                                      Mouse MARK3-associated protein #12.
                                                                                                                                                                                                      ADI29250 standard; protein; 296 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 170; 233pp;
                                                                                                                                                                                                                                                                                                                     gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dobie KW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JUN-2002; 2002US-00174319.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUN-2002; 2002US-00174319.
                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ward DT, Freier SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2004-052188/05.
                                                                                                                                                                                                                                                                                                                  Mouse; antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ADI29368
                                                                                                                                     269
                                                                                                           PL 345
                                                                                                                                                                                                                                                                                                                                                                                                                US2003232771-A1
                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                            22-APR-2004
                                                                                                                                     PL
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                                                                                                           344
                                                                                                                                     268
                          172
                                                                                                                                                                                                                                  ADI29250;
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ADI29250
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ABP62954 standard; protein; 358 AA.

ABP6295 RESULT

344 PL 345

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Human polypeptide SEQ ID NO 391.

(first entry)

14-OCT-2002

ABP62954;

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The invention relates to an isolated polynucleotide (I) comprising one of 245 sequences (ABD93288-ABQ93532). Treating a condition comprising administering to a mammalian subject a composition comprising the protein (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II). ((I) and (III) are useful for diagnostic evaluation of disorders. (I) is useful for gene therapy of diseases and (II) can be used for
                                                                                                                             Human; vulnerary; dermatological; neuroprotective; nootropic; cancer; antiparkinsonian; immunostimulant; cytostatic; immunosuppressive; antipalbetic; antiallergic; gene therapy; wound healing; tissue repair; burn; central nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; immune disorder; autoimmune disorder; multiple sclerosis; diabetes; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzheimer's, Parkinson's, Huntington's, amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID NO 391; 284pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ren F, Zhar
Wehrman T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhou P, Xue AJ,
u C, Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                  31-AUG-2001; 2001WO-US027093.
                                                                                                                                                                                                                                                                                                                                                                                01-SEP-2000; 2000US-00654935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Asundi V, Zh
Wang D, Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002-583321/62.
                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABQ93433.
                                                                                                                                                                                                                                                                                  WO200218424-A2.
                                                                                                                                                                                                                                                    domo sapiens.
                                                                                                                                                                                                                                                                                                                   07-MAR-2002.
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Zhao QA,
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therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's Hutington's and amylotrophic lateral sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from NIPO at from the patent directly from From Into at the printed specification, but was obtained ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 NCIHRDIKPENILITKQGIIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTQYG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 SSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human; cyclin-dependent kinase like 1; CDKL1; branching morphogenesis; branching morphogenesis modulator; angiogenic disorder; apoptotic disorder; proliferation disorder; chromosome 14.
                                                                                                                                                                                                                                                                                                                                                            1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 AVASQSAGITGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCL
                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cyclin-dependent kinase like 1 (CDKL1) protein SEQ ID NO:4
                                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                          63.9%; Score 1162.5; DB 5; Length 358; 63.8%; Pred. No. 1e-115; ive 42; Mismatches 46; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TI;
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Stott GM, Trowe T,
Jin Y, Hai B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPVDVWAIGCVFAELLSGVPLWPGKSDVDQLYLIRKTL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:|||| ||| ||| ||| HDPTERLTCEQLLHHPYFENIREIEDLAKEHNK 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 KMNPDDRLICSQLLESSYFDSFQEAQIKRKARNE 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plowman GD, Karim FD, Swimmer C,
Schulte-Merker S, Langheinrich U,
Odenthal JH, Scheel JK, Will TT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADO01538 standard; protein; 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-OCT-2002; 2002US-0420554P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-365563/34.
N-PSDB; ADO01535.
                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                     Sequence 358 AA;
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The present invention describes the use of a cyclin-dependent kinase like I (CDKLI) polypeptide or nucleic acid for modulating branching morphogenesis in a mammalian cell or for diagnosing a disease in a patient. Also described: (1) identifying a candidate branching morphogenesis modulating agent; (2) modulating branching morphogenesis modulating agent; (2) modulating branching morphogenesis modulating contacting the cell with an agent that specifically binds a CDKLI, polypeptide or nucleic acid; and (3) a method for diagnosing a disease in a patient. The CDKLI polypeptide or nucleic acid is useful for modulating branching morphogenesis in a mammalian cell. It is also useful for diagnosing a disease, e.g. andiogenic, apoptotic or proliferation disorder in a patient. The present sequence represent invention. The human CDKLI gene is located on chromosome 14, more
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCIHRDIKPENILITKQGIIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTQYG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSVDIWAIGCVFAELLTGOPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------GDLIPRHQQVFSTNQYFSGVKIPDPEDMEPLELKFPNISYPALGLKGCL 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
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Use of cyclin-dependent kinase like 1 polypeptides or nucleic acids for modulating branching morphogenesis in a mammalian cell or for diagnosing a disease e.g. angiogenic, apoptotic or proliferation disorder in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 AVASQSAGITGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cardiovascular disorder; hypertension; coronary artery disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein kinase; enzyme; cytostatic; osteopathic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.6%; Score 1157.5; DB 8 64.7%; Pred. No. 3.6e-115; tive 41; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 KMNPDDRLTCSQLLESSYFDSFQEAQ 325
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HMDPTERLTCEQLLHHPYFENIREIE
                                                                                                                                                                     Example; SEQ ID NO 4; 52pp; English.
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hes 211; Conservative
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as hypertension and coronary artery disease, and some endothelial cell disorders, including psoriasis. The current sequence represents a human kinase 14257 amino acid sequence
                                                                                                                                                              Query Match
Best Local Similarity
Matches 213; Conserv
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N-PSDB; AAF44669.
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                                                                                                                      AA;
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                                                                                                                      Sequence 228
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                  8 x 3 3 3 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16]. .218
/note= "kinase transferase protein serine/threonine-
protein ATP-binding II phosphorylation casein alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New 14257 polypeptides (protein kinases), useful as diagnostic targets and therapeutic agents for controlling cellular proliferative and/or differentiative disorder, bone disorders, immune disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "serine/threonine protein kinase active-site
                                                                                                                                                                                                                                                                                                                                                         "casein kinase II phosphorylation site"
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                                                                                                                                                                                                  "tyrosine kinase phosphorylation site"
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105. .208
                                                                                                                                                        'note= "eukaryotic protein kinase domain"
                                                                                                                                                                                                                                                                            .32
:e= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "casein kinase II phospl
188. .193
/note= "N-myristoylation site"
204. .211
                                                                                                                                                                                                                                                                                                                                                                                                           /note= "N-myristoylation site"
132. .134
                                                                                                                                                                                                                             .26
.e= "N-glycosylation site"
endothelial cell disorder; psoriasis
                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       signal site"
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                                                                                                                                                                                                                                                                                                                                                           'note=
                                                                                                                                                                                                          note=
                                                                                                                                                                                                                                                                                                              note=
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N-PSDB; AAI64248.
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                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers.
                                                                                                                                            PNLVNLIEVFRRKRKKKHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH
                                                                                                                                                                                                                                  1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                1 MGKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPIVKKIALREIRMLKQLKG
                                                                                                                                                                                                             NCIHRDIKPENILITKQGIIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTQYGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunosuppressive; cardiant; renal; antiinflammatory; antiaethmatic; dermatological; antidiabetic; antiinfertility; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis.
                                                  Gaps
                                                 ö
                 Length 228;
                                               Indels
                                                                                                                                                                                                                                                                                SVDIWAIGCVFAELLTGOPLWPGKSDVDQLYLIIRTL 217
                                                                                                                                                                                                                                                                                                     SVDIWAIGCVFARLITGQPLWPGKSDVDQLYLIRTL 217
            Score 1134; DB 5;
Pred. No. 5.9e-113;
2; Mismatches 2;
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62.3%; Sc._
98.2%; Pred
2; !
                                                                                                                                                                                                                                                                                                                                                                                                 AAB65642 standard; protein; 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10; Fig 1; 310pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-2000; 2000WO-US014842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                               Conservative
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27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                       149
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assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase antagonists may also be used to down regulate kinase
                                                                                                                                                                                                                                                                                                     275
                   and kinase antagonists may also be used to down regulate kinase expression and activity. Diseases related to kinase expression and activity Diseases related to kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative-stress related disorders, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
                                                                                                                                                                                                                                                        215
                                                                                                                                                                                                                                                                   DMETLEEKFSDVHPVALNFMKGCLKMNPDDRLTCSQLLESSYFDSFQEAQIKRKARNEGR 208
                                                                                                                                                                                                                                                                                                                            121 TL------GKLIPRHQSIFKSNGFFHGISIPEDE 148
                                                                                                                                                                                                                                                                                                                                                  DMETLEEKFSDVHPVALNFMKGCLKMNPDDRLJTCSQLLESSYFDSFQEAQIKRKARNEGR 335
                                                                                                                                                                                                                         1 NGVADGVIKSVLWQTLQALNFCHIHNCIHRDIKPENILITKQGIIKICDFGFAQILIFPGD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antisense compound targeted to a nucleic acid molecule encoding microtubule-affinity-regulating kinases (MARK3), useful for modulating
                                                                                                                                                                                                                                                                                                     TLVETGFRHVDQAGLELLTSSDPPAVASQSAGITGKLIPRHQSIFKSNGFFHGISIPEPE
                                                                                                                                                                                                           NGVADGVIKSVLWQTLQALNFCHIHNCIHRDIKPENILITKQGIIKICDFGFAQILIPGD
                                                                                                                                                                                                                                                          AYTDYVATRWYRAPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIR
                                                                                                                                                                                    34; Gaps
                                                                                                                                                            Score 1123; DB 4; Length 247;
Pred. No. 1e-111;
1; Mismatches 0; Indels 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; antisense gene therapy; MARK3;
MAP/Microtubule affinity-regulating kinase 3; or
Alzheimer's disease; neurodegenerative disorde;
hyperproliferative disorder; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADI29249 standard; protein; 247 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human MARK3-associated protein #37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dobie KW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JUN-2002; 2002US-00174319.
                                                                                                                                                             61.7%;
86.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUN-2002; 2002US-00174319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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NRRRQQNQLLPL 220
                                                                                                                                                                                                                                                                                                                                                                                                NRRRQ--QVLPL 345
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISIS-) ISIS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Freier SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-052188/05.
N-PSDB; ADI29367.
                                                                                                                                                                         Local Similarity
                                                                                                                                         Sequence 247 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS2003232771-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                   217;
                                                                                                                   disorders
                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                        156
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                                                                                                                                                                                                                                                                                                                                                                                                                     209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADI 29249;
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                                                                                                                                                                                     Matches
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The invention relates to a compound comprising a sequence comprising 8-80 base pairs (bp) targeted to a nucleic acid encoding MARK3 (MAP/microtubule affinity-regularing kinase 3), that specifically hybridises with the nucleic acid encoding MARK3 and inhibits expression of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a composition comprising the compound and a carrier or diluent, inhibiting the expression of MARK3 in cells or tissues, treating an animal having or suspected of having a disease or condition associated with MARK3 and screening for an antisense compound. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disorder, particularly cancer and neurodegenerative diseases e.g. Alzhelmer's disease. The present sequence is a MARK3 associated protein included in the figures but not mentioned anywhere else in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AYTDYVATRWYRAPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIR 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLVETGFRHVDQAGLELLTSSDPPAVASQSAGITGKLIPRHQSIFKSNGFFHGISIPEPE 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TL-----GKLIPRHQSIFKSNGFFHGISIPEPE 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 DMETLEEKFSDVHPVALNFMKGCLKMNPDDRLTCSQLLESSYFDSFQEAQIKRKARNEGR 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DMETLEEKFSDVHPVALNFMKGCLKANPDDRLTCSQLLESSYFDSFQEAQIKRKARNEGR 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 NGVADGVIKSVLWQTLQALNFCHIHNCIHRDIKPENILITKQGIIKICDFGFAQILIFGD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 NGVADGVIKSVLWQTLQALNFCHIHNCIHRDIKPENILITKQGIIKICDFGFAQILIPGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
expression of MARK3 or for treating cancer or Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1123; DB 8; Length 247; Pred. No. 1e-111; 1; Mismatches 0; Indels 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 16146.
                                                                      Disclosure; SEQ ID NO 169; 233pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB63118 standard; protein; 392 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.7%;
86.1%;
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11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2001; 2001WO-US009231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match . bl.,
Best Local Similarity 86.1
Matches 217; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NRRRQ--QVLPL 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NRRROQNOLLPL 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 247 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PEKE ) PE CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              specification.
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MDDT; human; disease detection and treatment molecule polypeptide; anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV; haemostatic; nephrotropic; antisnaemic; antipsoriatic; hepatotropic; gene therapy; protein replacement therapy; cell proliferative disorder; cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma; anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS; Goodpasture's syndrome; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human MDDT polypeptide SEQ ID 636,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABU11689 standard; protein; 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          psoriasis; hepatitis.
                N-PSDB; ABL07221
                                                                                                                                                                                  Sequence 392 AA;
                                                  interactions.
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                                                                                                                                                                                                  Query Match
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New purified disease detection and treatment molecule proteins and polymucleotides, useful for diagnosing, treating or preventing cancers (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis or hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID NO 636; 339pp + Sequence Listing; English.
                                                                                                                                 29-MAR-2001; 2001US-0280067P.
29-MAR-2001; 2001US-0280068P.
16-MAY-2001; 2001US-0291280P.
17-MAY-2001; 2001US-0291829P.
                                                                         27-MAR-2002, 2002WO-US009944
                                                                                                                                                                                                          17-MAY-2001; 2001US-0291849P.
19-JUN-2001; 2001US-0299428P.
20-JUN-2001; 2001US-0299776P.
                                                                                                                                                                                                                                                                    20-JUN-2001; 2001US-0300001P
                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                 Daugner.
Peralta CH, Davr.
T V. Marwaha R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ABX34679
 WO200279449-A2
                                                                                                             28-MAR-2001;
                                     10-OCT-2002
18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PNLVNLIEVFRRKRKAMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 PNLVSLLEVFRRKRRLHLVFEFCELTVLHELERHPQGCPEHLTKQICYQTLLGVAYCHKQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 NCIHRDIKPENILITKQGIIKICDFGFAQILIPGDAYIDYVATRWYRAPELLVGDTQYGS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GCLHRDIKPENILLTAQGQVKLCDFGFARMLSPGENYTDYVATRWYRAPELLVGDTQYGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 -----GDLLPRHIQIFGQNEYFKGITLFVPPTLEPLEDKMPAKSQQNPLTIDFLKK 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 VASQSAGITGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKF---SDVHPVALNFMKG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention iseful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), invention and the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 392;
                                                                                                                                       Disclosure; SEQ ID NO 16146; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 CLKMNPDDRLTCSQLLESSYFDSF ~- QEAQIKRKARNEGRNRRRQQV 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | :| | :| | :| :| | | | CLDKDPTKRWSCEKLTKHSYFDDYIAKQRELEHVNSLEAANLRQQQL 315
                                                                                                                                                                                                                                                                                                                                                                                                                             55.0%; Score 1001.5; DB 53.0%; Pred. No. 2.6e-98; rative 65; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 184; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin IH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
Marwaha R, Lo A, Lan RY, Urashka ME;

erty Sc, Dam TC, I

2003-058431/05.

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This invention describes a novel disease detection and treatment molecule polypeptide (MDDT) which has anti-inflammatory, immunosuppressive, osteopathic, cytostatic, anti-HTV, haemostatic, nephrotropic. Costeopathic, cytostatic, and hepatotropic activity. The polynucleotides and the polypeptides of the invention can be used for gene therapy, compared in replacement therapy and are useful for treating a variety of protein replacement therapy and are useful for treating a variety of diseases or conditions. These polypeptides or polynucleotides are particularly useful for diagnosing, treating or preventing cell particularly useful for diagnosing, treating or preventing cell compared in melanoma, myeloma or sarcoma), anaemia, (copin's disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's cyndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or copy ABUIL450-ABUIL450-ABUIL485 represent the MDDT polynucleotides encoded by ABUIL450-ABUIL450-ABUIL450-ABUIL461 in the disclosure of the invention. NOTE: The sequence data for this patent did not form part of the printed copy such particulation, but was obtained in electronic format from WIPO at the invention control compared to the printed copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy and copy
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Best Local Similarity
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SV 187

186

Homo sapiens

Search completed: April 22, 2005, 06:47:31 Job time : 101.447 secs

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20, Appl
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10, Appl
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Sequence 10, Application US/09671050

Patent No. 6716616

GENERAL INFORMATION:

APPLICANT: Donoho, Gregory

APPLICANT: Nehls, Michael

APPLICANT: Sands, Arthur T.

TITLE OF INVENTION: Polynucleotides Encoding the Same

FILE REFERENCE: LEX-0046-USA

CURRENT FILING DATE: 2001-06-11

PRIOR PAPLICATION NUMBER: US/09/671,050

CURRENT FILING DATE: 2001-06-11

PRIOR PAPLICATION NUMBER: US 60/156,511

PRIOR FILING DATE: 1999-09-28

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 347
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100.0%; Pred. No. 2.4e-186;
tive 0; Mismatches 0;
                         ALIGNMENTS
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ORGANISM: homo sapiens
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US-09-671-050-10
Query Match
Best Local S:
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Sequence 4, Appli
Sequence 12, Appli
Sequence 6, Appli
Sequence 11, Appl
Sequence 11, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 2, Appli
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1077, Ap
1013, App
25, Appl
25, Appl
26, Appl
17, Appl
115, Appl
115, Appl
115, Appl
116, Appl
                                                                                                     April 22, 2005, 04:37:19 ; Search time 34.071 Seconds (without alignments) 760.272 Million cell updates/sec
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                                                                                                                                                                                              1 MEKYEKLAKTGEGSYGVVFK.....RKARNEGRNRRRQQVLPLKS 347
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              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-411-628-4
US-10-174-794-4
US-09-949-016-7954
US-09-411-628-10
US-09-411-628-10
US-09-671-050-2
US-09-538-092-1236
US-09-949-016-0652
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US-09-417-197-115
US-09-411-628-13
US-10-174-794-13
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                                                                                                                                                                                                                                                                          513545 seqs, 74649064 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Score 1636; DB 4;
Pred. No. 1.1e-166;
0; Mismatches 0;
        ; FILE REFERENCE: LEX-0046-USA
CURRENT APPLICATION NUMBER: US/09/671,050
CURRENT FILING DATE: 2001-066-11
FRIOR APPLICATION NUMBER: US 60/156,511
PRIOR FILING DATE: 1999-09-28
NUMBER: OF SEQ ID NOS: 13
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 315
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
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Best Local Similarity 90.8
Matches 315; Conservative
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ORGANISM: homo sapiens
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Sequence 4, Application US/09671050

Sequence 1 NroRATION:
SEQUENCE INFORMATION:
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Triedrich, Glenn
APPLICANT: Exidency, Glenn
APPLICANT: Exidency, Glenn
APPLICANT: Exidency, Glenn
APPLICANT: Exidency, Glenn
APPLICANT: Exidency, Glenn
APPLICANT: Exidency
APPLICANT: Exidency
APPLICANT: Exidency
APPLICANT: Exidency
APPLICANT: Sande, Arthur T.
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE OF INVENTION: Polynucleotides Encoding the Same
CURRENT APPLICATION NUMBER: US/09/671,050

CURRENT FILING DATE: 2001-06-11

PRIOR APPLICATION NUMBER: US 60/156,511

PRIOR PELLING DATE: 1999-09-28

NUMBER OF SEQ ID NOS: 13

COFTWARE: FastSEQ for Windows Version 4.0
                                               347
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98.7%; Score 1796; DB 4; Length 356;
Best Local Similarity 100.0%; Pred. No. 9.2e-184;
Matches 342; Conservative 0; Mismatches 0; Indels
301 MNPDDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQQVLPLKS
                      Sequence 12, Application US/09671050
| Patent No. 6716616
| GENERAL INFORMATION:
| APPLICANT: Turner, C. Alexander Jr.
| APPLICANT: Turner, C. Alexander Jr.
| APPLICANT: Friedrich, Gienn
| APPLICANT: Friedrich, Gienn
| APPLICANT: Friedrich, Gienn
| APPLICANT: Sambrowicz, Brian
| APPLICANT: Sands, Arthur T.
| TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
| TITLE OF INVENTION: Polymucleotides Encoding the Same
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LENGTH: 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Sequence 6, Application US/09671050
| Patent No. 6716616
| Patent No. 6716616
| APPLICANT: Turner, C. Alexander Jr.
| APPLICANT: Turner, C. Alexander Jr.
| APPLICANT: Friedrich, Glem
| APPLICANT: Friedrich, Glem
| APPLICANT: Sambrowicz, Brian
| APPLICANT: Sambrowicz, Brian
| APPLICANT: Sambrowicz, Brian
| APPLICANT: Sambrowicz, Brian
| APPLICANT: Sambrowicz, Brian
| APPLICANT: Sambrowicz, Brian
| APPLICANT: Sambrowicz, Brian
| APPLICANT: Sambrowicz, Brian
| TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
| FILE REFERENCE: LES-0046-USA
| CURRENT FILING DATE: 2001-06-11
| PRIOR APPLICATION NUMBER: US/09/671,050
| PRIOR FILING DATE: 1999-09-28
Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 MNPDDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQQVLPLKS 347
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Pred. No. 4.2e-164;
0; Mismatches 0;
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Best Local Similarity 90.6
Matches 310; Conservative
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1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH 60

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61 PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWOTLQALNFCHIH 120
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64.7%; Pred. No. 2.6e-115;
tive 41; Mismatches 41; Indels 33;
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parent No. 6664066

GENERAL INFORMATION:
APPLICANT: University of Southern California
TITLE OF INVENTION: CDNA, GENONIC, AND PREDICTED PROTEIN
TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES;
FILE REFERENCE: 13761-707
CURRENT APPLICATION NUMBER: US/10/174,794
CURRENT PILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FESTESC for Windows Version 4.0
SEQ ID NO 11
                                                                                                                              Sequence 11, Application US/09411628

Patent No. 6428994

GENERAL INFORMATION:
APPLICANT: UNIVERSITY Of SOUthern California
TITLE OF INVENTION: EDNA, GENOMIC, AND PREDICTED PROTEIN
TITLE OF INVENTION: EDQUENCES OF LEARNING-INDUCED KINASES
FILE REFERENCE: 13761-707

CURRENT APPLICATION NUMBER: US/09/411, 628
CURRENT FILING DATE: 1999-10-01

BARLIER FPILING DATE: 1999-10-02

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FBSELSEQ for Windows Version 4.0

SEQ ID NO 11

LENGTH: 358
                           279 HWDPTERLTCEQLLHHPYFENIREIEDLAKEHNK 312
      300 KMNPDDRLTCSQLLESSYPDSFQEAQIKRKARNE 333
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270 HMDPTERLTCEQLLHHPYFENIREIE 295
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ORGANISM: Homo sapiens
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APPLICANT: VEXTER, J. Craig et al.
APPLICANT: VEXTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTERO FOR WINDOWS VERSION 4.0
SEQ ID NO 7552
LENGTH: 367
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1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
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                                                                                                                                                                                                                                                  301 MNPDDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQQV 342
                                                                                                                                                                                                                                                                                                                                                                                                                   269 MNPDDRLTCSQLLESSYFDSFQEAQIRRKARNEGRNRRRQQV 310
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Best Local Similarity 63.8
Matches 213; Conservative
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181 KAVDVWAIGCLVTEMLMGEPLFPGDSDIDQLYLIMRCL
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Best Local Similarity 49.7%
Matches 177; Conservative
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US-09-949-016-7954
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                                                                                                    33;
                                                                         Length 358;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence 4, Application US/09411628
; Patent No. 642894
; Patent No. 642894
; TUTLE NO. 642894
; TITLE OF INVENTION: EDNA, GENOMIC, AND PREDICTED PROTEIN
; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES; FILE REPERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/09/411,628
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: US 60/102,906
; BARLIER PILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FRIESCA FOR WINDOWS VERSION 4.0
                                                                                                    41; Indels
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                                                                    Score 1157.5; DB 4;
Pred. No. 2.6e-115;
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                                                                                               41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                300 KMNPDDRLTCSQLLESSYFDSFQEAQ 325
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; ORGANISM: Orcytolagus cuniculus
US-09-411-628-4
                                                                    tch 63.6%; al Similarity 64.7%; 211; Conservative 4:
             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-794-11
LENGTH: 358
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US-09-411-628-4
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Sequence 7954, Application US/09949016
Sequence 7954, Application US/09949016
Setent No. 681233
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: PILH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
240 AVASQSAGITGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCL 299
                            219 ------GNLIPRHQELFYKNPVFAGVRLPEIKESEPLERRYPKLSEVVIDLAKKCL 268
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                                                                                                                                                                                                                                                                                                                APPLICANT: University of Southern California
TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
FILE REPERENCE: 13761-707
CURRENT APPLICATION NUMBER: US/10/174,794
CURRENT FILING DATE: 2002-06-18
PRIOR PRICK FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FRSESEQ for Windows Version 4.0
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hes 65;
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49.7%; Pred. No. 7.4e-
tive 67; Mismatches
                                                                                                                                                                                                                                                      ; Sequence 4, Application US/10174794
; Patent No. 6664086
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180 SSVDIWAIGCVPAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
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271 HIDPDKRPFCAELLHHDFFQMDGFAERFSQELQLKVQKDARNVSLSKKSQNRKKEK 326
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TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
FILE REPERENCE: 13761-707
CURRENT APPLICATION NUMBER: US/09/411,628
CURRENT APPLICATION NUMBER: US 60/102,906
EARLIER APPLICATION NUMBER: US 60/102,906
NUMBER OF SEQ ID NOS: 16
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                                                          69;
                                                                                                                                                                                                                                                                                                                           Query Match 50.3%; Score 915.5; DB 4 Best Local Similarity 48.3%; Pred. No. 3.4e-89; Matches 172; Conservative 68; Mismatches 69
CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 7954
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; Patent No. 6428994
; GENERAL INFORMATION:
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US-09-411-628-10
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US-09-949-016-7954
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Best Local Simil
Matches 172; (
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TYPE: PRT
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240 AVASQSAGITGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCL 299
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                                                                                                                                                      1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
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Sequence 10, Application US/10174794

Patent No. 6664086

GENERAL INFORMATION:
TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
TITLE OF INVENTION: EDGUENCES OF LEARNING-INDUCED KINASES
FILE REFERENCE: 13764-707

CURRENT APPLICATION NUMBER: US/10/174,794

CURRENT FILING DATE: 1999-10-01

PRIOR PILING DATE: 1999-10-01

PRIOR APPLICATION NUMBER: US 60/102,906

PRIOR PILING DATE: 1999-10-01

PRIOR PILING DATE: 1999-10-02

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo sapiens
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LENGTH: 493
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US-10-174-794-10
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                                                                                     APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Gland
APPLICANT: Friedrich, Glann
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REPREMENT: 12x-0046-USA
CURRENT APPLICATION NUMBER: US/09/671,050
CURRENT APPLICATION NUMBER: US 60/156,511
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Donoblo, Gregory

APPLICANT: Towner, C. Alexander Jr.

APPLICANT: Towner, C. Alexander Jr.

APPLICANT: Towner, Glenn

APPLICANT: Friedrich, Glenn

APPLICANT: Sandsowicz, Brian

APPLICANT: Sandsowicz, Brian

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APPLICANT: Sandsowicz, Brian

APPLICANT: Sandsowicz, Brian

FILE REFERENCE: LEX-0046-USA

CURRENT FILING DATE: 1999-09-28

NUMBER OF SEQ ID NOS: 13

SOFFWARE: FastSEQ for Windows Version 4.0

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43.5%; Score 791; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 2e-76;
Matches 151; Conservative 0; Mismatches 0; Indels
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43.5%; Score 791; DB 4; PBest Local Similarity 100.0%; Pred. No. 1.8e-76; Matches 151; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 NCIHRDIKPENILITKOGIIKICDFGFAQIL 151
Sequence 2, Application US/09671050 Patent No. 6716616 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-671-050-8; Sequence 8, Application US/09671050; Patent No. 6716616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: homo sapiens
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TYPE: PRT
CRGANISM: homo sapiens
US-09-671-050-8
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 2
LENGTH: 187
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PNLVNLIBVFRRKRKMHLVFBYCDHTLLNELBRNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                                                                                                                                                                                                                61 PNLVNLIEVFRRKRRWHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1236, Application US/09538092

Sequence 1236, Application US/09538092

Sequence 1236, Application US/09538092

GENERAL INFORMATION:

APPLICANT: Mansfield, Traci A.

TITLE OF INFORMION: Protein-Protein Complexes and Method of Using Same;

TITLE OF INFORMION: Protein-Protein Complexes and Method of Using Same;

CURRENT FILING DATE: 1090-03-29

PRIOR PELICATION NUMBER: 60/127,352

PRIOR PELICATION NUMBER: 60/127,352

PRIOR PILING DATE: 1999-04-01

PRIOR APPLICATION NUMBER: 60/178,965

PRIOR PILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 1387

SOPTHARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPARE: CURRAPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 CHIHNCIHRDIKPENILITKQGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGD 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 TQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTS 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57
                                                                                       1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKOLKH
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... OTHER ... OTHER LINFORMATION: Polypeptide Accession Number Q00526.
US-09-538-092-1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 NFWKGCLKMNPDDRLTCSQLLESSYFDSFQEAQIKRK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
31.0%; Score 565; DB 4;
Best Local Similarity 36.8%; Pred. No. 6.5e-52;
Matches 124; Conservative 66; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 NCIHRDIKPENILITKQGIIKICDFGFAQIL 151
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Job time : 36.071 secs
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LOCATION: (0)...(0)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-538-092-1236
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US-10-766-691-10
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546.5
545.5
545.5
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Sequence 12, Appl
Sequence 10, Appl
Sequence 391, Appl
Sequence 97, Appl
Sequence 11, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 10, Appli
Sequence 10, Appli
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                                                                                                                                                             April 22, 2005, 06:50:50 ; Search time 859.637 Seconds (without alignments) 134.334 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                      US-10-766-691-10
1820
1 MEKYEKLAKTGEGSYGVVFK......RKARNEGRNRRRQQVLPLKS 347
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1: /cgn2 6/prodata/1/pubpaa/USO7 PUBCOMB.pep:*
2: /cgn2 6/prodata/1/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2 6/prodata/1/pubpaa/USO6 NEW_PUB.pep:*
5: /cgn2 6/prodata/1/pubpaa/USO6 NEW_PUB.pep:*
6: /cgn2 6/prodata/1/pubpaa/USO7 NEW_PUB.pep:*
7: /cgn2 6/prodata/1/pubpaa/USO8_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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7 US-10-766-691-12
5 US-10-333-314-10
7 US-10-333-314-10
7 US-10-366-691-6
US-10-366-61-97
1 US-10-664-421-97
1 US-10-64-421-97
1 US-10-174-794-11
US-10-174-794-10
1 US-10-174-794-10
1 US-10-174-794-10
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Maximum Match 100%
Listing first 45 summaries
                                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1162.5
1160.5
1157.5
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Perfect score:
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No.
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Sequence 544, App Sequence 115, App Sequence 115, App Sequence 115, App Sequence 115, App Sequence 11, App Sequence 51, App Sequence 7, App Sequence 55, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 133, Ap Sequence 134, App Sequence 13, App Sequence 13, App Sequence 13, App Sequence 13, App Sequence 13, App Sequence 13, App Sequence 103, App Sequence 104, App Sequence 1067, App Sequence 107, App Sequence 107, App Sequence 1087, App Sequence 1087, App Sequence 1087, App Sequence 1087, App Sequence 1087, App Sequence 1087, App Sequence 1087, App Sequence 1087, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, App Sequence 11, 
                                                                                                                                                                                                                                                      Sequence 187
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                                                                                                                                                                                                                                     US-09-771-161A-187

US-09-771-161A-187

US-10-174-13

US-10-295-681-51

US-10-295-681-51

US-10-295-681-51

US-10-295-681-51

US-10-295-681-14

US-10-295-681-14

US-10-295-681-14

US-10-295-681-39

US-10-295-681-39

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US-10-295-681-39
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ALIGNMENTS

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MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH 60
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                                                                                                                                                                APPLICANT: Durner, Gregory
APPLICANT: The Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Content of Co
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ilarity 100.0%; Pred. No. 3.6e-143;
Conservative 0; Mismatches 0;
Sequence 10, Application US/10766691
Publication No. US20050042626A1
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Best Local Similarity
Matches 347; Conservat
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Sequence 108, App

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301 MNPDDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQQV 342
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301 MNPDDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQQV
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Pred. No. 6.7e-128;
0; Mismatches: 0;
                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nehls, Michael
APPLICANT: Briefarch, Glenn
APPLICANT: Sands Arthur T.
ITILE OF INVENTION: Novel Human Kinase Proteins a:
ITILE OF INVENTION: Polymucleotides Encoding the
ITILE OF INVENTION: Novel Human Kinase Proteins a:
ITILE OF INVENTION: Polymucleotides Encoding the
ITILE OF INVENTION: Novels: 2004-01-28
ITILE APPLICATION NUMBER: US/09/671,050
FRIOR FILING DATE: 2000-09-27
FRIOR FILING DATE: 1990-09-27
FRIOR FILING DATE: 1990-09-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FARENSEQ for Windows Version 4.0
SEQ ID NO 12
                                                                                                                                                                                    Sequence 12, Application US/1076691
Publication No. US20050042626A1
GENERAL INFORMATION:
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US-10-766-691-12
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TYPE: PRT
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                   61 PNLVNLIEVFRKRKWHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH
                                                                                       NCIHRDIKPENILITKQGIIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTQYGS
                                                                                                                         SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA
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APPLICANT: DOUGHO, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Teadrich, Glenn
APPLICANT: Triedrich, Glenn
APPLICANT: Sands, Arthur T.
TILE OF INVENTION: Polymuclectides Encoding the Same
TILE REFERENCE: LEX-0046-0128
FILIE REFERENCE: LEX-0046-01-28
FRICH APPLICATION NUMBER: US/09/671,050
FRICH APPLICATION NUMBER: US 60/156,511
FRICH APPLICATION NUMBER: US 60/156,511
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FRICH APPLICATION NUMBER: US 60/156,511
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Publication No. US20050042626A1
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US-10-766-691-4
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Best Local Simi
Matches 342;
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121 NCIHRDIKPENILITKQGIIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTQYGS 180
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                                                                        Gaps
                                                                    32;
Length 315;
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                                                                    Indels
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Publication No. US20030211093A1
GENERAL INFORMATION:
APPLICANT: INCYTE GENOMICS, INC.; YUB, Henry
APPLICANT: KHAN, Farrah A.; GURURAJAN, Rajagopal
APPLICANT: HAFALIA, April J.A.; CHAWIA, Narinder K.
APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi
APPLICANT: GANDHI, Ameena R.; POLICKY, Jennifer L.
APPLICANT: GANDHI, Ameriah R.; TRIBOULEY, Catherine
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63.9%; Score 1162.5; DB 15; Length
Best Local Similarity 63.8%; Pred. No. 2e-88;
Matches 213; Conservative 42; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                  TITLE OF INVENTION: Novel Human Kinase Proteins and
TITLE OF INVENTION: Novel Human Kinase Proteins and
TITLE OF INVENTION: Polymucleotides Encoding the Same;
FILE REFERENCE: LEX-0046-USA;
CURRENT APPLICATION NUMBER: US/10/766,691
CURRENT AILING DATE: 2004-01-28
PRIOR PILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20040044181A1
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPRENCE: 2172-113 (793)
CURRENT APPLICATION NUMBER: US/10/363,616
CURRENT FILING DATE: 2003-03-03
PRIOR PELING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEO ID NOS: 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 88.6%; Score 1612; DB 17; Best Local Similarity 90.6%; Pred. No. 6.9e-126; Matches 310; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: homo sapiens
US-10-766-691-6
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-391
                       Zambrowicz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 -----GKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCLK 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 PNLVNLIEVFRRKRKKKHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
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88.6%; Score 1613; DB 15; Length 342;
Best Local Similarity 89.9%; Pred. No. 6e-126;
Matches 312; Conservative 1; Mismatches 0; Indels 34
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APPLICANT: THORNTON, Michael B.; BANDWAN, Olga APPLICANT: NGUYEN, Danniel B.; LU, Yan APPLICANT: BURRORD, Nell; LLL, Preeti G.; APPLICANT: DING, Li; YAO, Monique G. APPLICANT: DING, Li; YAO, Monique G. APPLICANT: ELLIOTI, Vicki S.; RECIPON, Shirley A. APPLICANT: GREENNELD, Sara R.; TANG, Y. Tom APPLICANT: GREENNELD, Sara R.; TANG, Y. Tom APPLICANT: GREENNELD, Sara R.; TANG, Y. Tom APPLICANT: GIETZEN, Kimberly J.; YANG, Junming APPLICANT: GIETZEN, Kimberly J.; YANG, Junming APPLICANT: JACKSON, Jennifer L.; TITLE OF INVERTION: HUMAN KINASES FILE REFERENCE: PI-0162 USN
GURRENT APPLICATION NUMBER: DS(10/333,314)
CURRENT FILING DATE: 2001-07-20
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-07-21
PRIOR PELICATION NUMBER: US 60/222,112
PRIOR FILING DATE: 2000-07-21
PRIOR FILING DATE: 2000-09-04
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 40
SOOTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 1698381CD1
US-10-333-314-10
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Publication No. US20050042626A1
GENERAL INFORMATION:
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nehls, Michael
APPLICANT: Priedrich, Glenn
APPLICANT: Priedrich, Glenn
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ORGANISM: Homo sapiens
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US-10-766-691-6
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Sequence 2, Application US/09834496A; Patent No. US20020090701A1; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: KAPATION:
; TITLE OF INVENTION: 14257 NOVEL PROTEIN KINASE MOLECULES AND
; TITLE OF INVENTION: THERR USES THEREFOR;
; FILE REFERENCE: 38152000900
; CURRENT APPLICATION NUMBER: US/09/834,496A;
; CURRENT FILING DATE: 2000-04-13
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOPTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                               APPLICANT University of Southern California
TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
FILE REFERENCE: 13761-707
CURRENT PAPLICATION NUMBER: US/10/174,794
FRIOR APPLICATION NUMBER: US/09/411,628
PRIOR APPLICATION NUMBER: US/09/411,628
PRIOR APPLICATION NUMBER: US 60/102,906
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: US 60/102,906
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1998-10-02
NUMBER OF SEQ. ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4.0
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                    300 KMNPDDRLTCSQLLESSYFDSFQEAQIKRKARNE 333
                                             63.6%; Score 1157.5; DB : 64.7%; Pred. No. 5.2e-88; ive 41; Mismatches 41
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Best Local Similarity 64.7%
Matches 211; Conservative
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ORGANISM: Homo sapiens
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                                           61 PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                    NCIHRDIKPENILITKQGIIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTQYG 179
                                                                                                                                                            SSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
                                                                                                                                                                                                                                                                                                                                      2 MEKYEKIGKIGEGSYGVVFKCRNRDTGQIVALKKFLESEDDPVIKKIALREIRMLKQLKH 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 SSVDIWAIGCVFABLLIGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
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Publication No. US20040142864A1
GENERAL INFORMATION:
APPLICANT: BERENER, RYAN
APPLICANT: KUNAR, ABHINN
APPLICANT: KUNAR, ABHINN
APPLICANT: MANDIYAN, VALSAN
APPLICANT: MILBURN, WICHAEL V.
TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
FILE REFERENCE: 039363/0703
CURRENT APPLICATION NUMBER: US/10/664,421
                                                                                                                                                                                                                                               300 KMNPDDRLTCSQLLESSYFDSFQEAQIKRKARNE 333
                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION WUNBER: 60/412,341
PRIOR FILING DATE: 2002-09-20
PRIOR FILING DATE: 2002-09-20
PRIOR FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 169
SOFTWARE: Patentin Ver. 3.2
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US-10-664-421-97
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US-10-664-421-97
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61 PNLVNLIEVFRRKKKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                                                                               121 NCIHRDIKPENILITKQGIIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTQYG 179
                                                                                                                                                                                                                                      180 SSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
                                                                                                                                                                                                                                                                                                                                                                                                              220 ------GDLIPRHQQVFSTNQYFSGVKIPDPEDMEPLELKFPNISYPALGLLKGCL 269
                                                               1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
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      Gaps
33;
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300 KMNPDDRLTCSQLLESSYF--DSF----QEAQIK--RKARN-----EGRNRRRQQ 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.3%; Score 915.5; DB 1. 48.3%; Pred. No. 1.1e-67; artive 68; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 22, Application US/10369022; Publication No. US20030203847A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 48.3
Matches 172, Conservative
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US-10-369-022-22
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Best Local Similarity 49.7%; Pred. No. 8.7e-70;
Matches 177; Conservative 67; Mismatches 65; Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10174794

Sequence 4, Application US/10174794

Publication No. US20030166220A1

GENERAL INFORMATION:

APPLICANT: University of Southern California

TITLE OF INVENTION: CDNA, GENOWIC, AND PREDICTED PROTEIN

TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES

FILE REFERENCE: 13761-707

CURRENT APPLICATION NUMBER: US/10/174,794

CURRENT FILING DATE: 2002-06-18

PRIOR APPLICATION NUMBER: US 60/102,906

PRIOR APPLICATION NUMBER: US 60/102,906

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENTH: 566
                                                                                         62.3%; Score 1134; DB 9; Length 228; 98.2%; Pred. No. 2.8e-86;
                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                      181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTL 217
                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Orcytolagus cuniculus US-10-174-794-4
                                                                                                          Best Local Similarity 98.2
Matches 213, Conservative
                   TYPE: PRT
ORGANISM: Homo sapiens
                                                     US-09-834-496A-2
 LENGTH: 228
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                                                                                         Query Match
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APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Rosenfeld, Julie Beth
APPLICANT: Rosenfeld, Julie Beth
APPLICANT: Rosenfeld, Julie Beth
APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
TITLE OF INVENTION: 12216, 17719, 41897, 44174, 33408, 10002, 16209, 314, 636,
TITLE OF INVENTION: 25431, 22245, 2387, 16658, 69112, 2188, 224, 615, 44372,
TITLE OF INVENTION: 13424 MOLECULES
TITLE OF INVENTION: 13424 MOLECULES
TITLE OF INVENTION: 13424 MOLECULES
CURRENT APPLICATION NUMBER: US/10/369,022
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269 HVDPDKRPPCAELLHHDFPQMDGFAERFSQELQMKVQKDARNISLSKKSQNRKKEK 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47;
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                                                                                                                                                       Sequence 10, Application US/10174794

Sequence 10, Application US/10174794

Publication No. US20030166220A1

GENERAL INFORMATION:

TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED RIVERING:

TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES

FILE REFERENCE: 13761-707

CURRENT APPLICATION NUMBER: US/10/174,794

CURRENT FILING DATE: 1999-10-01

PRIOR FILING DATE: 1999-10-01

PRIOR FILING DATE: 1999-10-02

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FRASERQ for Windows Version 4.0
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ORGANISM: Homo sapiens
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TYPE: PRT
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Publication No. US20040197825A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: Bilos-Santiago, Inmaculada
APPLICANT: Bilos-Santiago, Inmaculada
APPLICANT: Bilos-Santiago, Inmaculada
APPLICANT: Bilos-Santiago, Inmaculada
APPLICANT: Bilos-Santiago, Inmaculada
APPLICANT: Bilos-Santiago, Inmaculada
TITLE OF INVENTION: URCLOGICAL DISORDERS USING 44399, 54181, 211, 5687, 884,
TITLE OF INVENTION: 1055, 636, 4421, 5410, 30906, 2047,
TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44733, 51164,
TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PNLVNLIEVFRRKRRMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
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50.3%; Score 915.5; DB 15; Length 493;
Best Local Similarity 48.3%; Pred. No. 1.1e-67;
Matches 172; Conservative 68; Mismatches 69; Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: US 60/360,495
PRIOR FILING DATE: 2002-02-28
PRIOR PILING DATE: 2002-04-04
PRIOR PELICATION NUMBER: US 60/370,121
PRIOR PELING DATE: 2002-04-16
PRIOR FILING DATE: 2002-04-16
PRIOR FILING DATE: 2002-04-19
PRIOR FILING DATE: 2002-04-19
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2002-04-19
PRIOR PILING DATE: 2002-05-03
PRIOR PILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 60/377,717
PRIOR APPLICATION NUMBER: US 60/379,949
PRIOR APPLICATION NUMBER: US 60/382,409
PRIOR PILING DATE: 2002-06-03
PRIOR PILING DATE: 2002-06-03
PRIOR PILING DATE: 2002-06-04
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; ORGANISM: Homo sapiens
US-10-369-022-22
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32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423, 1515, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643, 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR 55053
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269 HIDFDKRPFCAELLHHDFFQMDGFAERFSQELQLKVQKDARNVSLSKKSQNRKKEK 324
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PRIOR PELLING DATE: 2003-01-15
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PRIOR PELLING DATE: 2003-02-04
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PRIOR PELLING DATE: 2003-02-07
PRIOR PELLING DATE: 2003-05-08
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PRIOR PELLING DATE: 2003-09-02
TITLE OF INVENTION: 32720, 4809, 14303, 1
TITLE OF INVENTION: 2158, 8263, 15402, 16
TITLE OF INVENTION: 2543, 9626, 13231, 33
TITLE OF INVENTION: 55053
TITLE OF INVENTION: 55053
CURRENT APPLICATION NUMBER: US/10/757,262
CURRENT FILING DATE: 2004-01-14
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APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nehls, Michael
APPLICANT: Priedrich, Glenn
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Publication No. US20050042626A1
GENERAL INFORMATION:
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Matches 172; Conservative
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Sequence 8, Application US/10766691

Publication No. USZO050042626A1

GENERAL INFORMATION:
APPLICANT: Donoho, Gregory
APPLICANT: Nehls, Michael
APPLICANT: Rededich, Glenn
APPLICANT: Sambrowicz, Brian
APPLICANT: Sambrowicz, Brian
APPLICANT: Sands, Arthur I.
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0046-USA
CURRENT FILING DATE: 2004-01-28
PRIOR APPLICATION NUMBER: US/09/671,050
PRIOR PLICATION NUMBER: US 60/156,511
PRIOR PLICATION NUMBER: US 60/156,511
PRIOR PLICATION NUMBER: US 60/156,511

PRIOR PLING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13

SOFTWARE: FASTERE for Windows Version 4.0

SEQ ID NO 8

LENGTH: 198

TAVED: DATE:
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Novel Human Kinase Proteins and
TITLE OF INVENTION: Novel Human Kinase Proteins and
TITLE OF INVENTION: Polymuclectides Encoding the Same
FILE REFERENCE: LEX-0046-USA
CURRENT FELING DATE: 1090-101-28
PRIOR APPLICATION NUMBER: US/09/671,050
PRIOR APPLICATION NUMBER: US 60/156,511
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 2
LENGTH: 187
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CRGANISM: homo sapiens
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1820
1 MEKYEKLAKTGEGGSYGVVFK.....RKARNEGRNRRRQQVLPLKS 347
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529 527.5 527.5 526.5 56		SULT 1 3.340 kinase (EC 2.7.1.37) cdc2-rel. Species: Homo sapiens (man) Date: 15-06-1994 #sequence_revisio Accession: S2333; S2244 Mccession: S23383; S2244 Mccession: S23383; S2244 Accession: S23383 Status nucleic acid sequence not si Molecule type: MRN Residues: 1-358 cMEY> Croses references: UNIPROT:Q0532; ES Superfamily: kinase rolated transfor Superfamily: kinase rolated transfor Superfamily: kinase colated transfor Accession: S2383 1-196 Medion: protein kinase homolo, 11-197 Medion: protein kinase APP-bi, 34,52,127,129/Active site: Lys, Glu Ouery Match I MEKYEKIAKTGEGSYGVVFKCRN I MEKYEKIAKTGEGSYGVVFKCRN	180 S
6		RESULT 1 S23318 is closed C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Accession: S2338; S224en E, Meyerson, M.; Enders, G.H.; EMBO J. 11, 2909-2917, 1992 A; Title: A family of human cd A; Reference number: S2338; A; Accession: S2338 A; Residues: 1-358 «MEX> A; Cession: S2338 A; Residues: 1-358 «MEX> A; Cession: S2388 A; Residues: 1-358 «MEX> A; Cession: S2388 A; Residues: 1-358 «MEX> A; Cession: S2388 A; Cession: S2388 A; Cession: Protein kinas F; 11-19, Mesdion: Protein kinas F; 11-19, Mesdion: Protein kinas F; 11-19, Mesdion: Protein kinas F; 11-19, Mesdion: Protein kinas F; 11-10, Mesdion: Protein kinas F; 11-10, Mesdion: Protein kinas F; 11-10, Mesdion: Protein kinas F; 11-10, Mesdion: Protein kinas F; 11-10, Mesdion: Protein kinas F; 11-10, Mesdion: Protein kinas F; 11-10, Mesdion: Protein kinas F; 11-10, Mesdion: Protein kinas F; 11-10, Mesdion: Protein kinas F; 11-10, Mesdion: Mesdicination A; Matches 211; Conservative Cy Fill	Vo qa

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Map position: 12413-12413
C, Superfamily: kinase-related transforming protein, protein kinase homology
C, Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein
C,2-255/Domain: protein kinase homology «KIN»
F;10-18/Region: protein kinase ATP-binding motif
F;10-18/Region: protein kinase ATP-binding motif
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Babo J. 11, 2909-2917, 1992
A;Title: A family of human cdc2-related protein kinases.
A;Reference number: S23382; MUID:92347325; PMID:1639063
                                                                                                                                                                                                                                                                                                                                                                                       7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -PGDAYTDYV 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATRWYRAPELLVGDIQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETG 221
                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                          C;Superfamily: kinase-related transforming protein; protein kinase homology C;Reywords: ATP; phosphotransferase; serine/threonine-specific protein kinase F;3-296/Domain: protein kinase homology «KIN»
F;11-19/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                 C;Species: Homo sapiens (man)
C;Date: 13-7an-1995 #sequence_revision 13-Jan-1995 #text_change 19-Dec-1997
C;Accession: S22745
R;Meyerson, M.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein kinase (EC 2.7.1.37) cdk3 - human
C;Species: Homo sapiens (man)
C;Date: 18-Jun-1993 #sequence_revision 18-Jun-1993 #text_change 09-Jul-2004
C;Accession: S23382, S22743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                               FRHVDQAGLELLTSSDPPAVASQSAGITGKLIPRHQSIFKSNGFFHGISIPEPEDMETLE
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                       51;
                                                                                                                                                                                                                                                                                                                                                    Length 376;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41; Indels
                                                                                                                                                                                                                                                                                                                                                    DB 2;
   protein kinase KKIALRE (EC 2.7.1.-)
                                                                                                                                                                                                                                                                                                                                                   Score 1149.5; DB
Pred. No. 5.7e-45;
                                                                                                                                                                                                                                                                                                                                                                                       41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCIHRDIKPENILITKQGIIKICDFGFAQILI--
                                                                                         submitted to the EMBL Data Library, May 1992
A;Reference number: S22743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                               63.2%;
                                                                                                                                                                                  A;Residues: 1-376 <MEY>
A;Cross-references: EMBL:X66359
                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 61.3%
Matches 211; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GDB:283456
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                                                                                                                                                                                                                                        A; Introns: 152/3; 170/3
                                                                                                                                              A; Status: preliminary A; Molecule type: mRNA
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                                                                                                                              A; Accession: S22745
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     serine/threonine
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C;Accession: 150474
C;Accession: 150474
C;Asdjura: H; Yamashita: M.; Katsu, Y.; Nagahama, Y.
Dev. Growth Differ: 35, 647-654, 1993
A;Title: Isolation and characterization of goldfish cdc2, a catalytic component of matura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P51958; GB:D17758; NID:9471097; PIDN:BAA04605.1; PID:g471098
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase
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                                                                                                                                                                                                                                                                                58 LKHPNIVRLLDVVHNERKLYLVFEFLSQDLKKYYMDSTPGSELPLHLIKSYLFQLLQGVSF 117
                                                                                                                                                                                                                                                                                                                                                                          CHIHNCIHRDIKPENILITKQGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGD 175
                                                                                                                                                                                                                                                                                                                                                                                                           176 TQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236 SDPPAVASQSA--GITGKLIPRHQSIFKSNGFFHGISIPEPE-DMETLEEKFSDVHPVAL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 HPNLVNLIEVFRRKRYMHLVFEYCDHTLLNELERNPNG--VADGVIKSVLWQTLQALNFC 117
                                                                                                                                                                                   57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein kinase (EC 2.7.1.37) cdc2 [similarity] - goldfish
C;Species: Carassius auratus (goldfish)
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
                                                                                                                                                             1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKF-VESEDDPVVKKIALREIRMLKQLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 HPNVVRLLDVIMQESKLYLVFEFLSMDLKKYLDSIPSGQFMDPMLVKSYLYQILEGILFC
                                                                                                                             MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKF---VESEDDPVVKKIALREIRMLKQ
                                                                                                                                                                                                                                                    LKHPNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNG-VADGVIKSVLWQTLQALNF
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                                                                   Gaps
                                                                   48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;2-25(Domain: protein kinase homology <KIN>
F;2-10-18/Region: protein kinase ATP-binding motif
F;33,51,128,130/Active site: Lys, Glu, Asp, Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30.9%; Score 563; DB 1; Length 302; 41.2%; Pred. No. 6.7e-19; ive 60; Mismatches 71; Indels
   Length 305;
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                                                             99; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 DLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQ 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  293 NFMKGCLKMNPDDRLTCSQLLESSYFDSFQEAQIKRK 329
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31.0%; Score 565; DB 2; 36.8%; Pred. No. 5.5e-19; iive 66; Mismatches 99;
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A;Molecule type: mRNA
A;Residues: 1-302 <KAJ>
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A; Molecule type: mRNA
A; Residues: 1-22, R., 94-297 < LEA>
A; Cross-references: BMB.:X14227; NID:g64665; PIDN:CAA32443.1; PID:g64666
R; Olive, M.; Theze, N.; Philippe, M.; Le Pennec, J.P.; Lerivray, H.
Gene 151, 81-88, 1994
A; Title: Cloning of the Xenopus laevis cdk2 promoter and functional analysis in oocytes &
A; Reference number: I51662; MUID:95129896; PMID:7828909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein ki
F;2-255/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
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R;Tsai, L.H.; Harlow, E.; Meyerson, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Ninomiya-Tsuji, J.; Nomoto, S.; Yasuda, H.; Reed, S.I.; Matsumoto, K. Proc. Natl. Acad. Sci. U.S.A. 88, 9006-9010, 1991
A;Title: Cloning of a human cDNA encoding a CDC2-related kinase by complementation of A;Reference number: A41227; MUID:92020980; PMID:1717994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 PNIVKLLDVIHTENKLYLVFEFLNQDLKKFMDGSNISGISLALVKSYLFQLLQGLAFCHS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HNCIHRDIKPENILITKQGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGDTQY 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---VETGFRHV----DQAGLELLTSSDPPAVASQSAGITGKLIPRHQSIFKSNGFFHGIS 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 PKWIRQDFSKVVPPLDEDGRDLLAQM---LQYDSNKRISAKVALTHP-----FFRDVS 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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C;Date: 17-Jul-1992 #sequence revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: A41227; S17873; S16520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:U07979; NID:g473584; PIDN:AAA82123.1; PID:g473585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90; Indels
                                                           A, Cross-references: UNIPROT: P23437; UNIPROT: Q9PSU0; GB:X14227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
30.5%; Score 555; DB 2;
Best Local Similarity 37.8%; Pred. No. 1.5e-18;
Matches 115; Conservative 59; Mismatches 90
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N;Alternate names: Eg1 homolog; protein kinase p34
                                                                                              R;le Guellec, R.
submitted to the EMBL Data Library, January 1989
A;Reference number: S15866
A;Accession: S15866
A;Molecule type: mRNA
A;Residues: 1-297 <PAR>
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A; Molecule type: mRNA
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A; Residues: 1-39 <OL
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N;Alternate names: cell division control protein CDC2 homolog Eg1
N;Alternate names: cell division control protein CDC2 homolog Eg1
C;Species Xenopus laevis (African clawed frog)
C;Date: 30-Apr-1991 #sequence revision 30-Apr-1991 #text_change 09-Jul-2004
C;Accession: A37871; S15866; ĪS1662; S14410
R;Paris, J.; Le Guellec, R.; Couturier, A.; Le Guellec, K.; Omilli, F.; Camonis, J.; Mad Proc. Natl. Acad Sci. U.S.A. 88, 1039-1043, 1991
A;Title: Cloning by differential screening of a Xenopus cDNA coding for a protein highly A;Reference number: A37871; MUID:91126051; PMID:1704128
                                                                                                                                                                                                                            R;Michaelis, C.E.; Weeks, G. submitted to the EMBL Data Library, August 1992
A;Description: The unicellular organism Dictyostelium discoideum possesses a highly rela
A;Reference number: $40021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Keywords: ATP; cell cycle control; phosphoprotein; phosphotransferase; serine/threonin P;2-254/Domain: protein kinase homology «KIN»
F;10-18/Region: protein kinase ATP-binding motif
F;33,51,126,128/Active site: Lys, Glu, Asp, Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Michaelis, C.; Weeks, G.
Jochim. Biophys. Acta 1179, 117-124, 1993
Title: The isolation from a unicellular organism, Dictyostelium discoideum, of a highl
Reference number: S39071; MUID:94032415; PMID:8218353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complex: In various organisms, cdc2 has been identified as a component of the M-phase Superfamily: kinase-related transforming protein; protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: UNIPROT: P34117; EMBL: L00652; NID: 9167695; PIDN: AAA16056.1; PID: 9167
                                                                         protein kinase (EC 2.7.1.37) cdc2 homolog - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S40021; S39071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 AVASQSAGITGKLIPRHQSIF-----KSNGFFHGISIPEPEDMETLEEKFSDVHPVALN 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 NCIHRDIKPENILITKQGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGDTQYG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MEXYSKIEKIGEGTYGIVNKAKORETGEIVALKRIRLDSEDEGVPCTAIREISLLKELKH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.7%; Score 558.5; DB 2; Length 292; 35.0%; Pred. No. 1e-18; tive 66; Mismatches 101; Indels 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294 FMKGCLKMNPDDRLTCSQLLESSYFDSFQ 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: mRNA
Residues: 1-18,'Y',20-188,'G',190-292 <MI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: EMBL:L00652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 35.0%
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    Status: preliminary
Molecule type: mRNA
Residues: 1-292 <MIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Status: preliminary
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Directin kinase (EC 2.7.1.37) cdc2 homolog 1 - rice C;Species: Oryza sativa (rice) C;Species: Oryza sativa (rice) C;Species: Oryza sativa (rice) C;Date: 13.7an-1995 #sequence_revision 13.7an-1995 #text_change 09-Jul-2004 C;Accession: S22440 Franchioto, J.; Hirabayashi, T.; Hayano, Y.; Hata, S.; Ohashi, Y.; Suzuka, I.; Utsugi, J. Mol. Gen. Genet. 233, 10-16, 1992 A;Tile: Isolation and characterization of CDNA clones encoding cdc2 homologues from Oryza, A;Reference number: S22440; MUID:92293101; PMID:1376401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P29618; EMBL:X60374; NID:g20342; PIDN:CAA42922.1; PID:g20343
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords. ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein ki
F;2-256/Domain: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                            61 PNLVNLIEVFRRKRKMHLVFEYCDHTLLN-----ELERNPNGVADGVIKSVLWQTLQAL 114
                                                                                                                                                                                                                                                                                                                                                                                                        VGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTL---VETGFRHVDQAG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 PNLVNLIEVFRRKRKMHLVFEYCDHTLLN-----ELERNPNGVADGVIKSVLWQTLQAL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 VGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLEL 232
kinase-related transforming protein; protein kinase homology
                                                                                                                                                                                                                                                                                                   115 NFCHIHNCIHRDIKPENILITKQ-GIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 LELLTSSDPPAVASQSAGITGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------PGVSCLPDFKTA--FPRWQA---------QDLATI---VPNLEP
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                                                                                                                                                                                                               53;
                                                                                                                                                          DB 2; Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 30.3%; Score 551.5; DB 2; Length 294; Best Local Similarity 34.8%; Pred. No. 2.2e-18; Matches 116; Conservative 68; Mismatches 102; Indels 47
                   C;Keywords: ATP; phosphotransferase

$2.256/Domain: protein kinase homology <KIN>

F;10-18/Region: protein kinase ATP-binding motif

F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;10-18/Region: protein kinase ATP-binding motif
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
                                                                                                                                                    30.4%; Score 552.5; DB 2; Length 35.4%; Pred. No. 1.9e-18; ive 66; Mismatches 98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 VALNFMKGCLKMNPDDRLTCSQLLESSYFDSFQEAQ 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 AGLDLLSKMLRYEPSKRITARQALEHEYFKDLEMVQ 294
                                                                                                                                                                                   Best Local Similarity 35.4
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Status: preliminary
A;Molecule type: DNA
A:Residues: 1-294 <HAS>
Superfamily:
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C; Stecies: 14-Feb-1199 #sequence_revision 14-Feb-1992 #text_change 28-Feb-1997
C; Accession: B44044
R; Colasanti, J.; Tyers, M.; Sundaresan, V.
Proc. Natl. Acad. Sci. U.S.A. 88, 3377-3381, 1991
A; Title: Isolation and characterization of CDNA clones encoding a functional p34(cdc2)
A; Reference number: A40444; MUID:91195354; PMID:2014258
                         adenovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A Map position: 12q13-12q13

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Keywords: ATP; call cycle control; mitosis; phosphoprotein; phosphotransferase;

E;2-255/Domain: protein kinase homology «KIN»

F;10-18/Region: protein kinase ATP-binding motif

F;14-16/Binding site: phosphate (Thr) (covalent) #status predicted

F;15/Binding site: phosphate (Tyr) (covalent) #status predicted

F;15/Binding site: phosphate (Tyr) (covalent) #status predicted
                                                                                                                                              A; Residues: 1-298 <TSA>
A; Cross-references: GB:X62071; NID:g312802; PIDN:CAA43985.1; PID:g312803
A; Cross-references: GB:X62071; NID:g312802; PIDN:CAA43985.1; PID:g312803
E; Elledge, S.J.; Spotteswood, M.R.
EMBO J. 10, 2653-2659, 1991
A; Title: A new human p34 protein kinase, CDK2, identified by complementation of A; Reference number: S16520; MUID:91330891; PMID:1714386
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181 STAVDIWSLGCIFAEMVTRRALFPGDSEIDQLFRIFRTLGTPDEVVWPGVTSMPDYKPSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
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                      cyclin A- and
                                                                                                                                                                                                                                                                                                                                          A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-176,'S',178-298 <ELL>
A.Cross-references: EMBL:X61622; NID:g29848; PIDN:CAA43807.1; PID:g29849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 PKWARQDFSKVVPPLDEDGRSLLSQMLHYDPNKRISAKAAL----
                   A;Title: Isolation of the human cdk2 gene that encodes the A;Reference number: S17873; WUID:91367262; PMID:1653904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.4%; Score 554; DB 2; 38.4%; Pred. No. 1.7e-18;
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Matches 118; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 GISIPEP 274
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A; Status: preliminary
A; Molecule type: mENA
A; Residues: 1-294 «COL»
A; Residues: GB: ME
                                                                                                    A;Status: preliminary
                                                                                                                              A; Molecule type: mRNA
                                                                        A;Accession: S17873
                                                                                                                                                                                                                                                                                                                    A; Accession: S16520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: GDB:CDK2
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Directal kinase (EC 2.7.1.37) cdc2 homolog A - maize C;Species: Zea mays (maize) C;Species: Zea mays (maize) C;Species: Zea mays (maize) C;Dacession: A40444 R;Colasanti, J.; Tyers, M.; Sundaresan, V. Proc. Natl. Acad. Sci. UC.3.A. 88, 3377-3381, 1991 Proc. Natl. Acad. Sci. UC.3.A. 88, 3377-3381, 1991 A;Title: Isolation and characterization of CDNA clones encoding a functional p34(cdc2) hc A;Reference number: A40444; MUID:91195354; PMID:2014258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ģ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 VGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLEL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 LISSDPPAVASQSAGITGKLIPRHQSIFKSNGFFHGIS-IP-----EPEDMETLEE 282
                                                                                  120 HNCIHRDIKPENILITKQ-GIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGDTQ 177
                                                                                                                                                                                                                                                    YGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIR---TLVETGFRHVDQAGLELLT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 SSDPPAVASOSAGITGKLIPRHOSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNF 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PNLVNLIEVFRKRKRKMHLVFEYCDHTLLN-----ELERNPNGVADGVIKSVLWQTLQAL 114
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                                     61 PNLVNLIEVFRKKKKMHLVFEYCDHTLLNELERNPNGVAD-GVIKSVLWQTLQALNFCHI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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A;Cross-references: GB:M60526
C;Superfamily: kinase-related transforming protein; protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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F2-256/Domain: protein kinase homology «KIN»
F;10-18/Region: protein kinase ATP-binding motif
F;30-18/Region: protein kinase ATP-binding motif
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 LSKMLLMDPTKRINARAALEHEYF 287
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Best Local Similarity 34.1?
Matches 117; Conservative
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A;Status: preliminary
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A; Residues: 1-294 < IMA>
A; Residues: 1-294 < IMA>
A; Residues: 1-294 < IMA>
A; Residues: 1-294 < IMA>
A; Cross-references: UNIPROT: P24100; EMBL: D10850; NID: 9217848; PIDN: BAA01623.1; PID: 92178
R; Inze, D.; Ferreira, P.; Hemerly, A.; Van Montagu, M.
B; Inze, D.; Ferreira, P.; Hemerly, A.; Van Montagu, M.
A; Title: Soc. Trans. 20, 80-84, 1992
A; Title: Control of cell division in plants.
A; Reference number: A48984; MUID: 92339744; PMID: 1634002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein kinase (BC 2.7.1.37) cdc2 - Arabidopsis thaliana
NyAlternate names: cdc2 protein homolog; CDC2a protein; cell division control protein 2
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: S23095; A48984; JQ1337; J000967; S18202
R;Imajuku, Y; Hirayama, T; Endoh, H; Oka, A.
A;Title: Exon-intron organization of the Arabidopsis thaliana protein kinase genes CDC2a
A;Reference number: S23095; MUID:92316202; PMID:1618302
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R;Hirayama, T.; Imajuku, Y.; Anai, T.; Matsui, M.; Oka, A.
Gene 105, 159-165, 1991
A;Title: Identification of two cell-cycle-controlling cdc2 gene homologs in Arabidopsis
A;Reference number: JQ1337; MUID:92039027; PMID:1937013
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                                                                                                                        233 LTSSDPPAVASQSAGITCKLIPRHQSIFKSNGFFHCISIPEPEDMETLEEKFSDVHPVAL 292
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224 -NEQSWPGVSS-----LPDYKSAFPK-----WQAQDLATI---VPTLDPAGL
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;Cross-references: GB:S45387; NID:g257373; PIDN:AAB23643.1; PID:g257374
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                                                                                                                                                                                                                                                                                     293 NFWKGCLKMNPDDRLTCSQLLESSYFDSFQEAQ 325
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 35.5
Matches 115; Conservative
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A, Experimental source: flower
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A;Map postition: 10q21.1-10q21.1
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; cell cycle control; mitosis; phosphoprotein; phosphotransferase; serine
F;2-256/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cycle
T49271

CELL DIVISION CONTROL PROTEIN 2 HOWOLOG A - Arabidopsis thaliana
NyAlternate names: protein T21J18.0
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000
C;Accession: T49271
R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Rudd, submitted to the Protein Sequence Database, April 2000
A;Reference number: Z25021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-297 <LEE>
A;Cross-references: UNIPROT:P06493; GB:X05360; NID:929838; PIDN:CAA28963.1; PID:929839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: A29539
R;Lee, M.G.; Nurse, P.
Nature 327, 31.35, 1987
A;Title: Complementation used to clone a human homologue of the fission yeast cell
A;Reference number: A29539; MUID:87201915; PMID:3553962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 YGSSVDIWAIGCVFAELLIGQPLWPGKSDVDQLYLIIR---TLVETGFRHVDQAGLELLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 SSDPPAVASQSAGIIGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein kinase (EC 2.7.1.37) cdc2 - human
N'Alternate names: cell division control protein 2 (CDC2)
C'Species: Homo sapiens (man)
C'Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43;
                                                                                                                                                                                                                                                                                                                                            A;Map position: 3
A;Introns: 3/3; 67/3; 105/3; 163/3; 218/2; 247/3; 265/3
C;Superfamily: kinase-related transforming protein; protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                          30.0%; Score 546.5; DB 2; Length 294; ilarity 35.2%; Pred. No. 3.6e-18; Conservative 71; Mismatches 96; Indels 43.
                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AL132963; GSPDB:GN00061; ATSP:T21J18.20
A;Experimental source: cultivar Columbia; BAC clone T21J18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 MKGCLKMNPDDRLTCSQLLESSYF 318
                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-294 <RIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                         A, Gene: ATSP: T21J18.20
                                                                                                                                                                                                       A; Status: preliminary
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Matches 114;
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protein kinase (EC 2.7.1.37) cdk2 [validated] - goldfish
C;Species: Carassius auratus (goldfish)
C;Species: Carassius auratus (goldfish)
C;Accession: A44878
R;Hirai, T.; Yamashita, M.; Yoshikuni, M.; Tokumoto, T.; Kajiura, H.; Sakai, N.; Nagahame
Dev. Biol. 152, 113-120, 1992
A;Title: Isolation and characterization of goldfish cdk2, a cognate variant of the cell of A;Reference number: A44878; MUID:92331802; PMID:1339936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Gene: cdk2
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Superfamily: kinase-related transforming; phosphoprotein; phosphotransferase; serine,
C;Keywords: ATP; cell cycle control; mitosis; phosphoprotein; phosphotransferase; serine,
F;2-255/Domain: protein kinase homology <KII».
F;10-18/Region: protein kinase ATP-binding motif
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rossidues: 1-298 cHIR>
A;Cross-references: UNIPROT:P43450; GB:S40289; NID:g251619; PIDN:AAB22550.1; PID:g251620
A;Experimental source: oocyte
A;Note: sequence extracted from NCBI backbone (NCBIN:108782, NCBIP:108783)
                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                        60 HPNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNG--VADGVIKSVLWQTLQALNFC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIHNCIHRDIKPENILITKQGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGDT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 TFPKWKPGSLASHVKNLDENGLDLLSKMLIYDP-----AKRISGKMALNH 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----VETGFRHVDQAGLELLTSS---DPPAVASQSAGITGKLIPRH 256
                                                                                                                                                                                          42;
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F;14,161/Binding site: phosphate (Thr) (covalent) #status predicte
F;15/Binding site: phosphate (Tyr) (covalent) #status predicted
F;33,51,128,130/Active site: Lys, Glu, Asp, Lys #status predicted
                                                                                                                               Length 297;
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                                                                                                                     29.9%; Score 545; DB 2; Length 29. 40.2%; Pred. No. 4.2e-18; ive 58; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 GSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTL 217
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-297 <YAN>
A;Residues: 1-297 <YAN>
A;Cross-references: UNIPROT:P48734; GB:L26547; NID:g433155; PIDN:AAA18894.1; PID:g498173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 HIHNCIHRDIKPENILITKQGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGDT 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cyclin-dependent kinase 1 - bovine (species: Bos primigenius taurus (cattle) (species: Bos primigenius taurus (cattle) (species: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004 (s.) Accession: 145971, c.E. Gene 141, 283-286, 1994 (a.) Title: Identification of cDNAs encoding bovine cyclin B and Cdkl/Cdc2. A.; Reference number: 145977; MUID:94215918; PMID:8163203
                                                                                                                                                                                                                                                                                                                                                                                   %,76me: cdk1/cdc2
C,Superfamily: kinase-related transforming protein; protein kinase homology
F;2-256/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.8%; Score 542; DB 2; Length 297;
40.2%; Pred. No. 5.7e-18;
tive 57; Mismatches 75; Indels 42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----VETGFRHVDQAGLELLTSS---DPPAVASQSAGITGKLIPRH 256
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Best Local Similarity 40.2*
Matches 117; Conservative
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GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR011009; Kinase like.
InterPro; IPR00179; Prot Kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR00221; Ser_thr_pkinase.
InterPro; IPR00221; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
FOROMOSI IPR00245; Tyr_pkinase.
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Q8ceq0 mus musculu
Q6qua0 homo sapien
Q66he7 rattus norv
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                                                                                                US-10-766-691-10
1820
1 MEKYEKLAKTGEGSYGVVFK.....RKARNEGRNRRRQQVLPLKS 347
                                                                                                                                                                                                                                                                                                                                                                                                       Description
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O76039 |
Q8wxq5 |
Q8bve0 r
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                        1612378 seqs, 512079187 residues
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Q8CEQQ
Q6CEQQ
Q6GHZ0
Q6GHZ1
C7QBG7
Q9UZH1
Q9VMN3
Q9TTKQ
Q9TTKQ
Q9Z772
Q9QX12
Q9QX12
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Q9QX11
Q6GMD6
Q6TXH3
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Maximum Match 100%
Listing first 45 summaries
                                      OM protein - protein search, using sw model
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Q8BL49
Q9JM02
Q9JM01
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Q9BMG2
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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length: 2000000000
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737.5
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Maximum DB seq
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MAN RRAU INLA ICDI ICDI MAN IXSA	ALIGNMENTS	PRT; 350 AA.	Created) Last sequence update) Last annotation update)	Name=zgc:101002; Brachydanio rerio (Zebrafish) (Danio rerio). Eukaryota; hetazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio. NCBI_TaxID=7955;	IISSUE=Embryo; 18.242603899;	A Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Honkins R.F., Jordan H., Moore T., Mang J., Haieh F.,	ner A.A., Rubin G.M., Hon Ido M.F., Casavant T.L., Shiyuki S., Carninci P.,	in K.J., Abraneon K.J., In K.J., Malek J.A., Guna S., Garcia A.M., Gay L.J. Gren E.J., Lu X., Gibbs	Madan A., Rodrigues S., Shevchenko Y., Bouffar	nmutz J., Myers R.M., But ailus D.E., Schnerch A.,	Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human	. U.S.A. 99:16899-16903 (2002).	SI2) SEQUENCE FROM N.A. STRAIN-SIngapore local strain; TISSUE-Embryo;	Director MGC Project; Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.	AAH79506.1; F:ATP binding; IEA.	s/threonine kinase activi
2 09%686 2 09%811 1 00%117 2 0661H7 2 0661H7 1 00%F5 2 070%F5 2 071%H7 2 071%H7 1 00%2 H7 1 00%2 H7 1 00%2 H7 1 00%2 H7 1 00%2 H7 1 00%2 H7 1 00%2 H7 1 00%2 H7 1 00%2 H7	~	id	28, Creat 28, Last 28, Last	fish) (I data; C) gii; Te]	train; 1 1073/pne	d B.A., S., Wac	K., Farm Bonal	A., Feur McKerne , Hale S	teman M ung A.C	J., SC!	analysi	.s.A. 9	train;	the EMBI	.1; nding;	n serine
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60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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                                                                                                                                        1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                                                    STRAIN=C57BL/63; TISSUE=Testis;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                 180 SSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP
                                                                                                                                                                                                                                                                                                             240 AVASQSAGITGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                       Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                      35;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Ol-MAR-2003 (TrEMBLrel. 23, Created)
Ol-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Ol-MAR-2004 (TrEMBLrel. 26, Last annoctation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4933411017 product:cyclin-dependent kinase-like 1
(CDC2-related kinase), full insert sequence.
                                                                                               65.0%; Score 1183.5; DB 2; Length 350; 63.4%; Pred. No. 1.9e-72; ive 47; Mismatches 45; Indels 35;
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                                                                                                                      45; Indels
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
                                                                          40810 MW; 9B04440EE0E38BE1 CRC64;
          SMART; SM00220; S_TKC; 1.

SMART; SM0019; TyrKC; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00101; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN 1.

SEQUENCE 350 AA; 40810 WW; 9804440EE0E33BEI
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  ProDom; PD000001; Prot_kinase; 1
                                                                                                                   220; Conservative
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                                                                                                       Similarity
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REQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE-Testis;

RA Adachi J., Alzawa K., Atahira S., Akimura T., Arai A., Aono H.,

RA Arakawa T., Bono H., Carninci B., Fukuda S., Fukunishi Y., Furuno M.,

RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

RA Kawai J., Kojima Y., Conno H., Saito H., Saito R., Sakai K.,

RA Saachi D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Saito R., Sakai K.,

RA Sogabe Y., Suzuki H., Tagami W., Tagawa A., Saito R., Shibata Y.,

RA Sogabe Y., Suzuki H., Tagami W., Tagawa A., Saito R., Sohino M.,

RA Sogabe Y., Suzuki H., Tagami Y., Shibata Y., Shinagawa A., Shiraka T.,

RA Sogabe Y., Suzuki H., Tagami Y., Shibata Y., Shinagawa A., Shiraka T.,

RA Submitted (JUL-2000) to the ENBL/GenBank/DDBJ databases.

BR MGJ: AKOIO7191 BAC25497.1; -.

BR MGJ: MGJ: 1918841; Cdkll.

BR MGJ: GO:00054648; P: Protein serine/threonine kinase activity; IEA.

GO: GO:0006468; P: Protein amino acid phosphorylation; IEA.

BR InterPro: IPR001109; Kinase.

BR InterPro: IPR001290; Ser_thr_pkinase.

BR InterPro: IPR002290; Ser_thr_pkinase.

BR Fam: PP00069: Pkinase: T.
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SEQUENCE FROM N.A.

SEQUENCE TROBLETESTIS;

MEDLINE=C57BJ/6J; TISSUB=Testis;

MEDLINE=C55BJ/6J; TISSUB=Testis;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yamamoto R., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Ishikawa T., Natoka M., Inoue Y., Kira A., Hayashizaki Y., Kawai J., Sequencing pipeline with 384 multicapillary sequencer.";
                                       STRAIN=C57BL/6J; TISSUE=Testis; MEDLIRE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., Wibitraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1830 (2000).
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SMART; SM00220; S_TKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE_DON; 1.
PROSITE; PS00108; PROTEIN KINASE_T; UNKNOWN_1.
ATP-binding; Cyclin; Kinase; Transferase.
SEQUENCE 352 AA; 41023 MW; 6E9F56C8080F35E0
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SEQUENCE FROM N.A
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RIASHORF R.D., Collins F.S., Wagner L., Sheamen C.W., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Sheafer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K. H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Stapleton M., Soares M.B., Parmer A.A., Rubin G.M., Hong L.,
Stapleton M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Robas S.A., McEwan P.J., McKerran K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Soedergren B.J., Lu X., Glübs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schwutz J.D., Myers R.M., Butterfield Y.S.,
A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
R. Jones S.J., Marra M.A.;
R. Jones S.J., Marra M.A.;
R. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
240 AVASQSAGITCKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCL
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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62.6%; Pred. No. 1e-70;
live 45; Mismatches 49; Indels 34
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SEQUENCE 352 AA; 40899 MW; DB9CDF5464E66E24 CRC64;
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Last annotation update)
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PROSITE; PSS0011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN 1.
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InterPro; IPR000719; Prot Kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
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SMART; SM00220; S_TKc; 1.
SMART; SM00219; TyrKc; 1.
                                                                                                                                                                                                                                                                                                                                       25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein
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Matches 214; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                             180 SSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
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                                                                                    240 AVASQSAGITGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Sherwood A.M., Leithauser B.J., Nickerson D.A.; Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AY255548; AAS00095.1; -.
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                                                                                                                                                                                                                       KMNPDDRLTCSQLLESSYFDSFQEA----QIKRKARNEGRNRRRQ----QVLP 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005524; F:ATP. binding; IEA.
GO; GO:0005524; F:ATP. binding; IEA.
GO; GO:0004713; F:protein serine/threonine kinase activity; IEA.
GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
GO; GO:0016740; F:rransferase activity; IEA.
GO; GO:0016468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR00179; Frot kinase.
InterPro; IPR00129; Fort kinase.
InterPro; IPR00129; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
FFGam; PF00069; Pkinase; I.
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SMART; SM00220; S_TKC; 1.
SMART; SM00219; TYKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN KINASE_DOM; 1.
ATP-binding; Cyclin; Kinase; Transferase.
SEQUENCE 358 AA; 41833 MW; 823E432BF84B77C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Cyclin-dependent kinase-like 1 (CDC2-related kinase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=CDKL1
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SEQUENCE FROM N.A.
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                                                                                                   120
                                                                                                                                                                              NCIHRDIKPENILITKQGIIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTQYG 179
                                                                                                                   SSVDIWAIGCVFAELLTGOPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
                                                                                                                                                                                                                                                                                                                                                        240 AVASQSAGITGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCL 299
                                                                                                                                                                                                                                                                                                                                                                                 219 ------GDLIPRHQQVFSMNQYFSGVKIPDPEDMETLELKFPNISYSALGFLKGCL 268
                  9
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                               PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH
           MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryoča, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harlow E., Tsai L.-H.;
"A family of human cdc2-related protein kinases.";
EMBO J. 11.2909-2917(1992)
-I. CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-I. SIMILARITY: Belongs to the Ser/Thr protein kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 603441; --
GO; GO:0004693; F:cyclin-dependent protein kinase activity; TAS.
GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
GO; GO:0000648; P:regulation of cell cycle; TAS.
InterPro; IPR011009; Kinase like.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR002290; Ser_thr_pkin_ase.
PF00069; Pkinase; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92347325; PubMed=1639063;
Meyerson M., Enders G.H., Wu C.-L., Su L.-K., Gorka C., Nelson
Harlow E., Tsai L.-H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Serine/threonine-protein kinase KKIALRE (EC 2.7.1.37) (Cyclin-dependent kinase-like 1).
                                                                                                                                                                                                                                                                                             300 KMNPDDRLTCSQLLESSYFDSFQE-AQIKRKARNEGRNRRRQ 340
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EMBL; X66359; CAA47002.1; JOINED.
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HSSP; P24941; 1H00.
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Q00532;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 SSVDIWAIGCVFAELLTGOPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterrygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                     33;
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                  DB 1; Length 358;
                                                                                                                                                                                            19 ATP (By similarity).
34 ATP (By similarity).
127 Proton acceptor (By similarity).
41834 MW, 88344321F24B77C6 CRC64;
ProDom; PD000001; Prot_kinase; 1.
SWART; SM00220; S TKG; 1.
SWOSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Serine/Chreonine-protein kinase; Transferase.
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004672; F:protein kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR011009; Kinase like.
InterPro; IPR000109; Prot kinase.
InterPro; IPR000119; Prot kinase.
InterPro; IPR0008271; Ser thr_pkin_AS.
Pfam; PF00069; Pkinase; I.
ProDom; PD000001; Prot_kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                     41; Indels
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                                                                                                                                                                                                                                                                                                                                Score 1157.5; DB
Pred. No. 1.1e-70;
                                                                                                                                                                  Protein kinase.
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Name=agCG55557; ORFNames=ENSANGG0000012213;
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                                                                                                                                                                                                                                                                                                                                                                                     41; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 KMNPDDRLTCSQLLESSYFDSFQEAQ 325
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EMBL; AAAB01008879; EAA08474.1; -.
                                                                                                                                                                                                                                                                                                                             63.6%;
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 64.7<sup>3</sup>
Matches 211, Conservative
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 ------GDLLPRHLAIFNQNEFFKGITLPVPPTLETLEAKMPSRTLANPLAMDFLKK 284
                                                                                                                                                                                                                                                                                                                             PNLVNLIEVFRRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                                                                                                                                                                                                                                                                                                                                                      121 NCIHRDIKPENILITKQGIIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTQYGS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 VASQSAGITGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSD---VHPVALNFMKG 297
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                                                                                                                                                                                                                                                            1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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Submitted (CGT-1998) to the EMBL/GenBank/DDBJ databases.

L. Submitted (CGT-1998) to the EMBL/GenBank/DDBJ databases.

R. EMBL; AL012618; CAB631367.1; -.

R. HSSP; P24941; LH00.

R. WormBase; WBGene00012779; Y42A5A.4.

R. WormBep; Y42A5A.4.; CE20258.

R. GO; 000005524; F:ATP binding; IEA.

R. GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004674; F:protein amino acid phosphorylation; IEA.

R. GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R. InterPro; IPR00109; Kinase like.

R. InterPro; IPR001299; Ser_thr_pkinase.

R. InterPro; IPR002290; Ser_thr_pkinase.

R. InterPro; IPR008271; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 CLKMNPDDRLTCSQLLESSYFDSF--QEAQIKRKARNEGRNRRRQQVLPLKS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || :| :| :: : : :| | : | CLDKDPAKRWSCERLATHPYFEDYITKQKEIEQTITLEQKQTGTRELKPKTS 336
                                                                                                                                                                                         37;
                                                                                                                                      55.5%; Score 1009.5; DB.2; Length 367; 52.8%; Pred. No. 1.3e-60; ive 62; Mismatches 67; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Genome seguence of the nematode C.elegans: A platform for
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS0011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN 1.
ATP-binding; Kinase; Transferase.
SEQUENCE 367 AA; 42402 MW; F23BDB4C5D28A5E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
11-MAY-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein Y42A5A.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      investigating biology.";
Science 282:2012-2018(1998)
                                                                                                                                                            Best Local Similarity 52.8 Matches 186; Conservative
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                                                                                                                                           Query Match
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WEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandaell M.D., Zhang Q., Chen L.X., Bandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., Handon R.C., Bayers E.G., Helt G., Nelson C.R., Gabor G.L., Am K.H., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Ballew R.M., Basu A., Barman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Bortier P., Rotchan M.R., Bulke C., Davengort L.B., Davies P., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P., Cherry J.M., Cawley S., Dahlke C., Davengort L.B., Davies P., Davibin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Rosler C., Gabriellan A.E., Gong F., Gorrell J.H., Gai S., Guna P., Harris M., Gladek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.L., Harvey D., Heiman T.J., Wei M.H., Ibegwam C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 PNLVNLIEVFRKRKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 353;
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63; Indels
Prodom; PD000001; Prot kinase; 1.
SMART; SM00220; S_TKc; 1.
PROSITE; PS00107; PROTEIN KINASE APP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN 1.
ATP-binding; Hypothetical protein; Kinase; Transferase.
SEQUENCE 353 AA; 40665 MW; 7E32260D9849CAC9 CRC64;
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Last annotation update)
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Best Local Similarity 53.4%; Pred. No. 4.3e-60;
Matches 187; Conservative 59; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2004 (TrEMBLrel. 26,
CG7236-PA.
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RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Rammel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lai Z., Lei Y., Lei Y., Levitz S., Kulp D., Lai Z., Lai Z., Lai Z., Lai Z., Lai Z., Lai Z., Lai Z., Lai Z., Lai Z., Lai Z., Lai Z., Lai Z., Lai X., Lai X., Lai X., Lai X., Lai X., Lai X., Lai X., Lai X., Lai X., Lai X., Lai X., Lai X., Lai X., Lai X., Lai X., Lai X., Lai X., Lai X., Lai X., Lai X., Lai X., Lai X., Lai X., Lai X., Lai X., Lai X., Lai X., McDherson D., McDherson D., Monnt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ra Melson K., Nalon K., Nalon S., Pollard J., Puri V., Reese M.G., Rainston K., Siden-Kiamos I., Simpson M., Skupski M. P., Smith T., Shue B.C., Stadling A.C., Stadlen-Kiamos I., Simpson M., Strong R., Sun E., Spradling A.C., Stagleton M., Strong R., Sun E., Suriskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wansaman D.A., Weinstock G.M., Weissenbach J., Williams S.M., WoodageT, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Rhong X.H., Mang Z.Y., Mang Z.Y., Wang Z.Y., Wang Z.Y., Wang Z.Y., Zhan M., Zhang G., Zhao Q.; Zheng L., Zheng X.H., Myers E.W., Rubin G.M., Venter J.C.; The Genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-22426065; PubMed=12537568; Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Glbbs R.A., Rubin G.M., "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDIJINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise B., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003611; AAF52279.1; -.
HSSP; P24941; 101Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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InterPro; IPR01009; Kinase like.
InterPro; IPR000719; Prot Kinase.
InterPro; IPR0082290; Ser Ihr Dkinase.
InterPro; IPR008271; Ser Ihr Dkinase.
Ffam; PF00069; Pkinase; I.
SMART; SM00220; S TKC; I.
PROSITE; PS00107; PROTEIN_KINASE_ATP; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 VASQSAGITGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKF---SDVHPVALNFMKG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218 ------GDLLPRHIQIFGQNEYFKGITLPVPPTLEPLEDKMPAKSQQNPLTIDFLKK 268
                                                                                                                                                                                                                                                                    1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH 60
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--- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL, ABO29045; BAA88508.1; --
HSSP; P24941; 101Q.
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PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS001107; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SEQUENCE 566 AA; 64052 MW; 5D57595550902EA9 CRC64;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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GO; GO:0004674; F:ATP binding; IEA.
GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
InterPro; IPR01009; Kinase like.
InterPro; IPR00719; Prot kinase.
InterPro; IPR002290; Sor thr pkinase.
InterPro; IPR00221; Sor thr pkinase.
From FP00069; Pkinase; I.
From FP000069; Pkinase; I.
From FP000069; Pkinase; I.
                                                                                                                                                                                                                37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 CLKMNPDDRLTCSQLLESSYFDSF--QEAQIKRKARNEGRNRRRQQV 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 CLDKDPTKRWSCEKLTKHSYFDDY1AKQRELEHVNSLEAANLRQQQL 315
                                                                                                                                                                                                                61; Indels
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN_1.
ATP-binding; Kinase; Transferase.
SEQUENCE 392 AA; 44962 MW; C9627D077784ES5D CRC64;
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181 PVDVWAIGCLFAELVRGEALWPGRSDVDQLYLIRKTL------
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Ser/Thr kinase KKIAMRE.
                                                                                                                                                  ; Score 1001.5; DB 2;
; Pred. No. 4.9e-60;
65; Mismatches 61;
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Best Local Similarity
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61 PNLVNLIEVFRKKRKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
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                                                                                                                                                                           182 VDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPAV 241
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MEDLINE=97152547; PubMed=9000130;
Taglienti C.A., Wysk M., Davis R.J.;
"Molecular cloning of the epidermal growth factor-stimulated protein kinase p56 KKIAMRE.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Last annotation update)
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48.3%; Pred. No. 4.3e-54;
tive 68; Mismatches 69
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Matches 172; Conservative
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                                                                                                                                61 PNLVNLIEVFRKKKKMHLVFEYCDHTLLNELERNPNGVADGVIKSVLWOTLQALNFCHIH 120
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Seo H.C., Edvardsen R.B., Maeland A.D., Bjordal M., Jensen M.F.,

A Hansen A., Flaat M., Weissenbach J., Lehrach H., Wincker P.,

Reinhardt R., Chourrout D.;

Thox cluster disintegration with persistent anteroposterior order of expression in Oikopleura dioica.";

Rature 431:67-71(204).

Rature 431:67-71(204).

REMBL, AY49462; AAS1447.1;

ROG 60:0016301; Frianse activity; IEA.

InterPro; IPR01009; Kinase like.

InterPro; IPR01009; Striase.

InterPro; IPR002290; Ser Ehr pkinase.

InterPro; IPR002291; Ser Ehr pkinase.

RITHERPRO; IPR002291; Ser Ehr pkinase.

InterPro; IPR002291; Ser Ehr pkinase.

InterPro; IPR002291; Ser Ehr pkinase.

RITHERPRO; IPR002295; Tyr pkinase.
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                                                                      1 MEKYENLGLVGEGSYGWYMKCRNKDSGRIVAIKKFLESDDDKWYKKIAMREIKLLKQLRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 KMNPDDRLTCSQLLESSYF--DSF----QEAQIK--RKARN-----EGRNRRRQQ 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oikopleura dioica.
Bukaryota, Metazoa, Chordata, Urochordata, Appendicularia,
Oikopleuridae, Oikopleura.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62; Indels
    65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385 AA; 45512 MW; 059F814421A6ADA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Cyclin-dependent kinase-like 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.2%; Score 932; DB 2; 52.2%; Pred. No. 2.5e-55; ative 58; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN 1.
CPC11n; Kinase.
SEQUENCE 385 AA; 45512 WW; 059F814421A6ADA1
    67; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00069; Pkinase; T.
ProDom; PD000001; Prot kinase; 1.
SMART; SM00220; S TKC; 1.
SMART; SM00219; TyrKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
    177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORFNames=006-03;
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Matches
    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
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121 NCIHRDIKPENILITKOGIIKICDFGFAQIL-IPGDAYIDYVATRWYRAPELLVGDTQYG 179
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                                                                                          298 CLKWNPDDRLTCSQLLESSYF--DSF----QEAQIK--RKARN-----EGRNRRRQQ 341
                                                                                                                              RP SEQUENCE FROM N.A.

RP STRAIN=129/SvJ, and C57BL/6; TISSUE=Brain;

RC STRAIN=129/SvJ, and C57BL/6; TISSUE=Brain;

RL SABSET T., Gondl H., Sun W., Ikeda T., Thompson R.F., Itohara S.;

RL SABSET T., Gondl H., Sun W., Ikeda T., Thompson R.F., Itohara S.;

RL SABSET T., Gondl H., Sun W., Ikeda T., Thompson R.F., Itohara S.;

RL SIMILARITY: Belongs to the Ser/Thr protein kinase family.

BREMI; AB029073; BAA88439.1; JOINED.

BREMI; AB029070; BAA88439.1; JOINED.

BREMI; AB029071; BAA88439.1; JOINED.

BREMI; AB029072; BAA88439.1; JOINED.

BREMI; AB029072; BAA88439.1; JOINED.

BREMI; AB029074; Prept binding; IEA.

BREMI; AB029075; Prept binding; IEA.

BREMI; AB029079; Cdkl2.

BREMI; AB029079; Rinase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

GO; GO:0016740; F:transferase activity; IEA.

BROSTER: PROMOTI9; Prote kinase.

InterPro; IPROMOTI9; Prot kinase.

InterPro; IPROMOTI9; Prot kinase.

InterPro; IPROMOSI; Frot kinase.

InterPro; IPROMOSI; Frot kinase.

REMRI; SMO0220; STKC; I.

ROSTE; PSOMO10; PROTEIN KINASE DOW; I.

PROSITE; PSOMO10; PROTEIN KINASE ATP; I.

ROSTER; PSOMO10; PROTEIN KINASE ST; I.

ROSTER; PSOMO10; RAINASE, SET; I.

ROSTER; PSOMO10; RAINASE, SET; I.

RAP-binding; Kinase; Serime threspective transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MEKYENLGLVGEGSYGWYMKCRNKDSGRIVAIKKFLESDDDKMVKKIAMREIKLLKQLRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 SSVDIWAIGCVFAELLIGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLISSDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49.7%; Score 904.5; DB 2; Length 5
48.6%; Pred. No. 2.8e-53;
cive 66; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 13, Last sequence update) Ser/Thr kinase KKTAMRE (Ser/Thr kinase KKTAMRE (Ser/Thr kinase KKTAMRE-beta) Name=cdkl2; Synonyms=Kkm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 KAVDIWAIGCLVIEMLMGQPLFPGESDIDOLHHIMTCL---
                PRT;
                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 48.6
Matches 174; Conservative
                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                              219
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180 SSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
                                                                  218
                                                                                                                      299
                                                                                                                                         -----GNLIPRHQELFNKNPVFAGVRLPEIKEREPLERRYPKLSEVVIDLAKKCL 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ENLVNLLEVCKKKKRRWYLVPEFVDHTILDDLKLFPNGLDYQVVQKYLPQIINGIGFCHSH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCIHRDIKPENILITKQGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGDTQYG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 SSVDIWAIGCVFAELLIGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLISSDPP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218
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                                                                                                        240 AVASQSAGITGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCL
                                                                                                                                                                                                              300 KMNPDDRLTCSQLLESSYF--DSF----QEAQIK--RKARN-----EGRNRRRQQ 341
                                                                                                                                                                                                                                                  269 HIDPDKRPFCAELLHHDFFQMDGFAERFSQELQLKVQKDARNVSLSKKSQNRKKEK 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRAIN-C57BL/6; TISSUE-Brain;
STRAIN-C57BL/6; TISSUE-Brain;
Strain-C57BL/6; TISSUE-Brain;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

LOUD STRAIN-C57BL/6; TISSUE-Brain;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.

LOUD STRAIN-C57BL/GEN-C58BASSUS, CO.

REMBL; AB029066; BAA88428.1; ---
REMBL; AB029066; BAA88428.1; ---
REMBL; AB029066; BAA88428.1; ---
REMBL; AB029066; BAA88428.1; ---
REMBL; AB029066; BAA88428.1; ---
REMBL; AB029066; BAA88428.1; ---
REMBL; AB029066; BAA88428.1; ---
REMBL; AB0290654; F:Protein serine/threonine kinase activity; IEA.

GO; GO:0006468; P:Protein amino acid phosphorylation; IEA.

GO; GO:0006468; P:Protein amino acid phosphorylation; IEA.

RICEPPRO; IPR000799; Prot kinase.

InterPro; IPR000799; Prot kinase.

InterPro; IPR002799; Ser_thr_pkinase.

REFAM; PF00069; Pkinase; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; Fuluever, S. TKC; 1.

PRART; SM01220; S. TKC; 1.

PROSITE; PS00101; PROTEIN KINASE ATP; 1.

PROSITE; PS00108; PROTEIN KINASE DOM; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.

ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

564 AA; 63640 MW; DACDEF630CCE82D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Ser/Thr kinase KKIAMRE-gamma.
                                 69
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49.7%; Score 904.5; DB 2
Best Local Similarity 48.6%; Pred. No. 2.8e-53;
Matches 174; Conservative 66; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                          564 AA
                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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ProDom; PD000001; Prot kinase, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Cdkl2; Synonyms=Kkm;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                               219
                                                                                                                                                                                                                                                                                                                                                                      Q9QYI2
ID Q9QYI2
AC Q9QYI2;
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Gaps

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RESULT 15
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61 PNLVNLIEVFRRKRKWHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 NCIHRDIKPENILITKQGIIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGDTQYG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 AVASQSAGITGKLIPRHQSIFKSNGFFHGISIPEPEDMET--LEEKFSDVHPVALNFMKG 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLKMNPDDRLTCSQLLESSYF--DSF-----QEAQIK--RKARN-----EGRNRRRQQ 341
                                                1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 SSVDIWAIGCVFABLLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73; Indels 44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          ATP-binding, Kinase; Serine/threonine-protein kinase; Transferase.
NON_TER 329 329
                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                        GG; GG:0005524; F:ATP binding; IEA.
GG; GG:0004674; F:ATP binding; IEA.
GG; GG:0004674; F:protein serine/threonine kinase activity; IEA.
GG; GG:0006468; P:protein amino acid phosphorylation; IEA.
InterPro; IPR011009; Kinase like.
InterPro; IPR00219; Prot kinase.
InterPro; IPR00229; Ser_thr_pkinase.
InterPro; IPR00229; Ser_thr_pkinase.
InterPro; IPR00829; Ser_thr_pkinase.
FREM: PF0069; Pkinase; I.
                                                                                                                                                                                                                          49.6%; Score 902; DB 2; Length 329;
49.0%; Pred. No. 2.3e-53;
tive 63; Mismatches 73; IndelB '
                                                                                                                                                                                                                                                                                                                                                                                                                                            329 AA; 38023 MW; F72EB89E65AE8585 CRC64;
                                                                                                                               Last sequence update)
                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Last sequence
01-OCT-2003 (TrEMBLrel. 25, Last annotati
Ser/Thr kinase KKIAMRE-delta (Fragment).
                                                                                                                                                                                                                                                                                                                                                                           Probom, PD000001; Prot kinase; 1.
SMART; SM0220; S TKc; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE OM; 1.
                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                         Name=Cdkl2; Synonyms=Kkm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 49.0%
Matches 173; Conservative
                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                 MGD; MGI:1858227; Cdkl2.
                                                                                                                                                                    Mus musculus (Mouse)
                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                     090YII
                                                                                   RESULT 14
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TISSUE=Kidney,

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

REDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RETAUSDENG R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Astalecon M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahesley J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rayakanski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                     269 CLHIDPDKRPFCADLLRHDFPQMDGPAERFSQELQLKIEKDARNNSLPKKSQK 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298 CLKMNPDDRLTCSQLLESSYF--DSF----QEAQIK--RKARNEGRNRRRQQ
                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                  320 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR011009; Kinase like.
InterPro; IPR00219; Prot Kinase.
InterPro; IPR00229; Ser Thr Dkinase.
InterPro; IPR008271; Ser thr Dkin AS.
InterPro; IPR001245; Tyr Dkinase.
Pfam; PF00069; Pkinase; I.
                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last seq
05-JUL-2004 (TrEMBLrel. 27, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD000001; Prot_kinase; 1.
SMART; SM00220; S_TKc; 1.
SMART; SM00219; TyrKc; 1.
                                                                                                                                                                                                                                                                                                                                                                                             LOC443693 protein (Fragment).
Name=LOC443693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopodinae; Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8355;
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61 ENLVNLLEVCKKKKKRWYLVFEFVDRTVLDDLEQFPNGLDFNRVRKYLFQIIRGIGFCFNH 120
                                                                                                                                                                                                                                                                                                                                                                NCIHRDIKPENILITKQGIIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTQYG 179
                                                                                                                                                                                                                                                                                                                                                                                        180 SSVDIWAIGCVFAELLIGOPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
                                                                                                                                                                                                                                                                                       61 PNLVNLIEVFRKKRKRKHLVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCHIH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 AVASQSAGITGKLIPRHQSIFKSNGFFHGISIPEPEDMETLEEKFSDVHPVALNFMKGCL 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 -----CQGNLTPRHQELFYRNPMFAGVSLPDMKEAESLERRYPKHSPVMLDLAKSCL 268
                                                                                                                                                                                                             1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVVAVKKFVESEDDPVVKKIALREIRMLKQLKH 60
                                                                                                                                                                                                                                   49.4%; Score 899; DB 2; Length 320;
48.8%; Pred. No. 3.5e-53;
tive 64; Mismatches 75; Indels 38; Gaps
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
NON TER 320 320
SEQUENCE 320 AA; 37063 MW; 4CD2189603F9115F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 KMNPDDRLTCSQLLESSYF--DSFQE---AQIKRKARNEGRNRRRQ 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 HIDPEKRPACGTLLQHELFTKDNFSERFSQEIRAKLQNLSKDNSSQ 314
                                                                                                                                    Query Match
Best Local Similarity 48.8%
Matches 169; Conservative
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Search completed: April 22, 2005, 06:50:39 Job time : 98.2054 secs